

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:51:18 ; Search time 4501 Seconds  
(without alignments)  
578.093 Million cell updates/sec

Title: US-10-604-726A-8797  
Perfect score: 252  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 15754707 seqs, 5162687648 residues

Total number of hits satisfying chosen parameters: 22946898

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:  
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21: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
22: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	32	12.7	32	11	US-10-536-560-26233
C 3	32	12.7	32	11	US-10-536-560-175427
C 4	32	12.7	32	11	US-10-536-560-325266
C 5	32	12.7	32	11	US-10-536-560-388542
C 6	32	12.7	32	11	US-10-536-560-390712
C 7	29	11.5	29	11	US-10-536-560-399537
C 8	29	11.5	116	21	US-11-443-428A-328462
C 9	25.4	10.1	64	19	US-11-130-645A-206881
C 10	25.4	10.1	64	19	US-11-130-645A-676631
C 11	25.2	10.0	103	21	US-11-443-428A-567727

C 12	24.8	9.8	113	21	US-11-443-428A-626563
C 13	24.2	9.6	63	19	US-11-130-645A-109784
C 14	24.2	9.6	63	19	US-11-130-645A-445004
C 15	24.2	9.6	63	19	US-11-130-645A-446298
C 16	24.2	9.6	64	19	US-11-130-645A-22287
C 17	24.2	9.6	64	19	US-11-130-645A-169416
C 18	24.2	9.6	64	19	US-11-130-645A-348741
C 19	24.2	9.6	64	19	US-11-130-645A-689158
C 20	23.8	9.4	63	19	US-11-130-645A-498699
C 21	23.8	9.4	64	19	US-11-130-645A-245318
C 22	23.8	9.4	64	19	US-11-130-645A-455660
C 23	23.8	9.4	114	21	US-11-497-489A-250527
C 24	23.8	9.4	115	21	US-11-497-489A-201561
C 25	23.6	9.4	64	19	US-11-130-645A-628544
C 26	23.6	9.4	97	12	US-10-708-951-59270
C 27	23.6	9.4	117	20	US-11-503-243A-338191
C 28	23.4	9.3	100	11	US-10-546-139A-1
C 29	23.4	9.3	106	21	US-11-443-428A-709830
C 30	23.4	9.3	115	21	US-11-443-428A-515014
C 31	23.2	9.2	64	19	US-11-130-645A-524987
C 32	23.2	9.2	64	19	US-11-130-645A-538342
C 33	23.2	9.2	81	11	US-10-536-560-457
C 34	23	9.1	63	19	US-11-130-645A-122147
C 35	23	9.1	64	19	US-11-130-645A-44883
C 36	23	9.1	64	19	US-11-130-645A-132874
C 37	23	9.1	64	19	US-11-130-645A-311109
C 38	23	9.1	64	19	US-11-130-645A-325285
C 39	23	9.1	64	19	US-11-130-645A-415331
C 40	23	9.1	64	19	US-11-130-645A-613037
C 41	23	9.1	64	19	US-11-130-645A-715805
C 42	23	9.1	64	19	US-11-130-645A-726268
C 43	23	9.1	64	19	US-11-130-645A-745478
C 44	23	9.1	65	19	US-11-130-645A-728884
C 45	23	9.1	83	13	US-11-635-706-14106

## ALIGNMENTS

RESULT 1  
US-10-536-560-26233/c  
; Sequence 26233, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATICALY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 06087.0300.PCUI3  
; CURRENT APPLICATION NUMBER: US/10/536,560  
; CURRENT FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 424571  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 26233  
; LENGTH: 32  
; TYPE: RNA  
; ORGANISM: Homo Sapiens  
US-10-536-560-26233

Query Match 12.7%; Score 32; DB 11; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 CTCTGGCCCCCTTAATGTACTTCGGGCTCGTA 229  
Db 32 CTCTGGCCCCCTTAATGTACTTCGGGCTCGTA 1

RESULT 2  
US-10-536-560-38260/c  
; Sequence 38260, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
 ; TITLE OF INVENTION: GENES AND USES THEREOF  
 ; FILE REFERENCE: 06087.0300.PCUS13  
 ; CURRENT APPLICATION NUMBER: US/10/536,560  
 ; CURRENT FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 424571  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 38260  
 ; LENGTH: 32  
 ; TYPE: RNA  
 ; ORGANISM: Homo Sapiens  
 US-10-536-560-38260

Query Match 12.7%; Score 32; DB 11; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 162 GCATCGCGCAGGAGGCGGGGAGACGA 193  
 Db 32 GCATCGCGCAGGAGGCGGGGAGACGA 1

RESULT 3

US-10-536-560-175427/c  
 ; Sequence 175427, Application US/10536560  
 ; Publication No. US20060257851A1  
 ; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD  
 ; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
 ; TITLE OF INVENTION: GENES AND USES THEREOF  
 ; FILE REFERENCE: 06087.0300.PCUS13  
 ; CURRENT APPLICATION NUMBER: US/10/536,560  
 ; CURRENT FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 424571  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 175427  
 ; LENGTH: 32  
 ; TYPE: RNA  
 ; ORGANISM: Homo Sapiens  
 US-10-536-560-175427

Query Match 12.7%; Score 32; DB 11; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TGAGGGGCTGTTAAGCGTCCCAAGTTG 46  
 Db 32 TGAGGGGCTGTTAAGCGTCCCAAGTTG 1

RESULT 4

US-10-536-560-325266/c  
 ; Sequence 325266, Application US/10536560  
 ; Publication No. US20060257851A1  
 ; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD  
 ; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
 ; TITLE OF INVENTION: GENES AND USES THEREOF  
 ; FILE REFERENCE: 06087.0300.PCUS13  
 ; CURRENT APPLICATION NUMBER: US/10/536,560  
 ; CURRENT FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 424571  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 325266  
 ; LENGTH: 32  
 ; TYPE: RNA  
 ; ORGANISM: Homo Sapiens  
 US-10-536-560-325266

Query Match 12.7%; Score 32; DB 11; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 CGCCTGAGTTTGAGCCAGACAGCTCGCAG 165  
 Db 32 CGCCTGAGTTTGAGCCAGACAGCTCGCAG 1

RESULT 5

US-10-536-560-388542/c  
 ; Sequence 388542, Application US/10536560  
 ; Publication No. US20060257851A1  
 ; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD  
 ; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
 ; TITLE OF INVENTION: GENES AND USES THEREOF  
 ; FILE REFERENCE: 06087.0300.PCUS13  
 ; CURRENT APPLICATION NUMBER: US/10/536,560  
 ; CURRENT FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 424571  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 388542  
 ; LENGTH: 32  
 ; TYPE: RNA  
 ; ORGANISM: Homo Sapiens  
 US-10-536-560-388542

Query Match 12.7%; Score 32; DB 11; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 CTCCTCTGCCACGGGCTGAGTTCCGGCTCC 121  
 Db 32 CTCCTCTGCCACGGGCTGAGTTCCGGCTCC 1

RESULT 6

US-10-536-560-390712/c  
 ; Sequence 390712, Application US/10536560  
 ; Publication No. US20060257851A1  
 ; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD  
 ; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
 ; TITLE OF INVENTION: GENES AND USES THEREOF  
 ; FILE REFERENCE: 06087.0300.PCUS13  
 ; CURRENT APPLICATION NUMBER: US/10/536,560  
 ; CURRENT FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 424571  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 390712  
 ; LENGTH: 32  
 ; TYPE: RNA  
 ; ORGANISM: Homo Sapiens  
 US-10-536-560-390712

Query Match 12.7%; Score 32; DB 11; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 TTGCTTCTCTTTTCTGGATGCAGATCCCTCTG 88  
 Db 32 TTGCTTCTCTTTTCTGGATGCAGATCCCTCTG 1

RESULT 7

US-10-536-560-399537/c  
 ; Sequence 399537, Application US/10536560  
 ; Publication No. US20060257851A1  
 ; GENERAL INFORMATION:

; APPLICANT: ROSETTA GENOMICS LTD  
 ; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
 ; TITLE OF INVENTION: GENES AND USES THEREOF  
 ; FILE REFERENCE: 06087.0300.PCUS13  
 ; CURRENT APPLICATION NUMBER: US/10/536,560  
 ; CURRENT FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 424571

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 399537
; LENGTH: 29
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-536-560-399537

Query Match      11.5%; Score 29; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 GGATGACAGTCTCTGACTCCCTCTGCC 100
Db 29 GGATGACAGTCTCTGACTCCCTCTGCC 1

RESULT 8
US-11-443-428A-328462
; Sequence 328462, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanging
; APPLICANT: Danari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 328462
; LENGTH: 116
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-443-428A-328462

Query Match      11.5%; Score 29; DB 21; Length 116;
Best Local Similarity 61.0%; Pred. No. 1.2e+03;
Matches 47; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 168 GGGCAGGAGGGGGGGGAGAGAGCGGCTCTGGCCCTTAATTGTTACTTCGGGCTCG 227
Db 29 GTGATGGAGAGAGGGTGTGGACTTTGGAGACTGGGTCAATAGGCGCACTCGGGTTCC 88

Qy 228 TATTGCTCTCTCTTCG 244
Db 89 TCCTGTGCTCTCTCTCG 105

RESULT 9
US-11-130-645A-206881
; Sequence 206881, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; FILE REFERENCE: 06087,0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 676631
; LENGTH: 64
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; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 206881
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-206881

Query Match      10.1%; Score 25.4; DB 19; Length 64;
Best Local Similarity 47.1%; Pred. No. 9.3e+03;
Matches 24; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 46 GGAAGGGCGCTTTGCTTCTGTTTCTGATGAGAGTCTCTGACTCCCTC 96
Db 14 GAAUGCGGCUUGUCUAGCAGCUCCUAGCUGUGUCUCCUCCUC 64

RESULT 10
US-11-130-645A-676631
; Sequence 676631, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; FILE REFERENCE: 06087,0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 676631
; LENGTH: 64
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## RESULT 14

US-11-130-645A-445004  
; Sequence 445004, Application US/11130645A  
; Publication No. US20070050146A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Amir, Avniel  
; APPLICANT: Yael, Karov  
; APPLICANT: Ranit, Aharonov  
; TITLE OF INVENTION: MicroRNAs and Uses Thereof  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130,645A  
; CURRENT FILING DATE: 2005-05-16  
; PRIOR APPLICATION NUMBER: PCT/US05/16986  
; PRIOR FILING DATE: 2005-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,577  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,572  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 60/666,340  
; PRIOR FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: US 60/665,094  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/662,742  
; PRIOR FILING DATE: 2005-03-17  
; PRIOR APPLICATION NUMBER: US 60/593,329  
; PRIOR FILING DATE: 2005-01-06  
; PRIOR APPLICATION NUMBER: US 60/593,081  
; PRIOR FILING DATE: 2004-12-08  
; PRIOR APPLICATION NUMBER: US 60/522,860  
; PRIOR FILING DATE: 2004-11-15  
; PRIOR APPLICATION NUMBER: US 60/522,457  
; PRIOR FILING DATE: 2004-10-04  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 760616  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 445004  
; LENGTH: 63  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-130-645A-445004

Query Match 9.6%; Score 24.2; DB 19; Length 63;  
Best Local Similarity 49.1%; Pred. No. 1.9e+04;  
Matches 26; Conservative 9; Mismatches 18; Indels 0; Gaps 0;  
Qy 125 TTCGCGTGTGCGCCCTGAGGTTTGAGGCCACAGCTCGCAGTCGGCGAGGAG 177  
Db 11 UUCUUGGUUCCUGAGGUUUCAGGCACUAAAAACUCUAUGUGGGGAAGGGAG 63

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US-11-130-645A-446298  
; Sequence 446298, Application US/11130645A  
; Publication No. US20070050146A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Amir, Avniel  
; APPLICANT: Yael, Karov  
; APPLICANT: Ranit, Aharonov  
; TITLE OF INVENTION: MicroRNAs and Uses Thereof  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130,645A  
; CURRENT FILING DATE: 2005-05-16  
; PRIOR APPLICATION NUMBER: PCT/US05/16986  
; PRIOR FILING DATE: 2005-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,577  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,572  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 60/666,340  
; PRIOR FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: US 60/665,094

; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/662,742  
; PRIOR FILING DATE: 2005-03-17  
; PRIOR APPLICATION NUMBER: US 60/593,329  
; PRIOR FILING DATE: 2005-01-06  
; PRIOR APPLICATION NUMBER: US 60/593,081  
; PRIOR FILING DATE: 2004-12-08  
; PRIOR APPLICATION NUMBER: US 60/522,860  
; PRIOR FILING DATE: 2004-11-15  
; PRIOR APPLICATION NUMBER: US 60/522,457  
; PRIOR FILING DATE: 2004-10-04  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 760616  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 446298  
; LENGTH: 63  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-130-645A-446298  
Query Match 9.6%; Score 24.2; DB 19; Length 63;  
Best Local Similarity 49.1%; Pred. No. 1.9e+04;  
Matches 26; Conservative 9; Mismatches 18; Indels 0; Gaps 0;  
Qy 125 TTCGCGTGTGCGCCCTGAGGTTTGAGGCCACAGCTCGCAGTCGGCGAGGAG 177  
Db 11 UUCUUGGUUCCUGAGGUUUCAGGCACUAAAAACUCUAUGUGGGGAAGGGAG 63  
Search completed: June 19, 2007, 15:43:23  
Job time : 4502 secs

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:14:19 ; Search time 2229 Seconds  
(without alignments)  
7814.408 Million cell updates/sec

Title: US-10-604-726A-8797  
Perfect score: 252  
Sequence: 1 ggggtatctgcaactgagag.....tctctcttttggccacctcc 252

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 4052000

Minimum DB seq length: 0  
Maximum DB seq length: 120

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27.8	11.0	98	5	S69137 Homo sapien
C 2	26.2	10.4	98	5	S89198 Homo sapien
C 3	25.2	10.0	109	7	AB150733 Homo sapi
C 4	24.8	9.8	92	2	AX900201 Sequence
C 5	24.8	9.8	92	2	BD035734 Sequence
C 6	24.8	9.8	92	2	AR735995 Sequence
C 7	24.6	9.8	103	2	C0471292 Sequence
C 8	24.6	9.8	104	2	CQ480460 Sequence
C 9	24.4	9.7	119	5	AY751306 Homo sapi
C 10	24.2	9.6	96	2	AR431314 Sequence
C 11	23.8	9.4	78	2	AR477180 Sequence
C 12	23.8	9.4	78	2	AR606935 Sequence
C 13	23.8	9.4	78	2	AR701924 Sequence
C 14	23.6	9.4	72	2	AX899202 Sequence
C 15	23.6	9.4	72	2	BD034735 Sequence
C 16	23.6	9.4	72	2	AR734996 Sequence
C 17	23.6	9.4	97	2	AX184498 Sequence
C 18	23.4	9.3	100	2	AX989552 Sequence

19	23.4	9.3	100	2	AX996400
20	23.4	9.3	100	2	CQ874706
C 21	23.2	9.2	59	2	E37929
C 22	23.2	9.2	81	10	AY390010
C 23	23.2	9.2	101	2	CQ149122
C 24	23.2	9.2	101	2	CQ232396
C 25	23.2	9.2	101	2	CQ307710
C 26	23.2	9.2	101	2	CQ344556
C 27	23.2	9.2	111	5	HS012224
C 28	23	9.1	51	6	AF094482
C 29	23	9.1	65	6	AY177451
C 30	23	9.1	65	2	BD461670
C 31	23	9.1	65	2	CQ531157
C 32	23	9.1	81	10	AF040860
C 33	23	9.1	120	7	BV012636
C 34	22.8	9.0	60	2	BD477333
C 35	22.8	9.0	60	2	CQ546820
C 36	22.8	9.0	110	5	HSRETINT11
C 37	22.6	9.0	66	2	CQ630945
C 38	22.6	9.0	66	2	AR472008
C 39	22.4	8.9	60	6	MUSIGXYZ
C 40	22.4	8.9	98	6	AF387673
C 41	22.4	8.9	119	2	AX907922
C 42	22.4	8.9	119	2	BD043455
C 43	22.4	8.9	119	2	AR743716
C 44	22.2	8.8	51	2	CQ007958
C 45	22.2	8.8	67	2	AX899414

#### ALIGNMENTS

RESULT 1  
S69137/c 98 bp mRNA linear PRI 16-MAR-2001  
LOCUS Homo sapiens T-cell receptor alpha-chain (TCR V alpha) mRNA,  
DEFINITION partial cds.  
ACCESSION S69137  
VERSION S69137.1 GI:545967  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Mohapatra,S., Mohapatra,S., Yang,M., Ansari,A.A., Parronchi,P.,  
Magli,E. and Romagnani,S.  
TITLE Molecular basis of cross-reactivity among allergen-specific human T  
cells: T-cell receptor V alpha gene usage and epitope structure  
JOURNAL Immunology 81 (1), 15-20 (1994)  
PUBMED 7510663  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 144559] from the original journal article.  
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Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 65 GTTTTCTGGATGACAGTCTCTGACTCCCTCTGCGACGGGTGAGTTTCGGGTCCAGG 124
DB 93 GATATTTGGCTTCACAGTGAGGTGAGTCCCAAGGTTGATTTCCTGCAATTGCT 34

QY 125 TTCGGGTGTCGCTCCCTGAGGTTTGAGGC 151
DB 33 GGTGCTTCTGCACAGAAGTAGGTGGC 7

RESULT 2
LOCUS S69198/c
DEFINITION Homo sapiens T-cell receptor alpha-chain (TCR V alpha) mRNA,
partial cds.
ACCESSION S69198
VERSION S69198.1 GI:545963
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 98)
AUTHORS Mohapatra,S.S., Mohapatra,S., Yang,M., Ansari,A.A., Parronchi,P.,
Maggi,E. and Romagnani,S.
TITLE Molecular basis of cross-reactivity among allergen-specific human T
cells: T-cell receptor V alpha gene usage and epitope structure
JOURNAL Immunology 81 (1), 15-20 (1994)
PUBMED 7510663
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 144557] from the original journal article.
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Matches 49; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 65 GTTTTCTGGATGACAGTCTCTGACTCCCTCTGCGACGGGTGAGTTTCGGGTCCAGG 124
DB 93 GATATTTGGCTTCACAGTGAGGTGAGTCCCAAGGTTGATTTCCTGCAATTGCT 34

QY 125 TTCGGGTGTCGCTCCCTGAGGTTTGAGGC 151
DB 33 GGTGCTTCTGCACAGAAGTAGGTGGC 7

RESULT 3
LOCUS AB150733
DEFINITION Homo sapiens DNA, STS on chromosome 10, D10S08121, sequence tagged
site.
ACCESSION AB150733

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VERSION AB150733.1 GI:62171551
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tamiya,G., Shinya,M., Imanishi,T., Ikuta,T., Makino,S., Okamoto,K.,
Furugaki,K., Matsumoto,T., Mano,S., Ando,S., Nozaki,Y., Yukawa,W.,
Nakashige,R., Yamaguchi,D., Ishibashi,H., Yonekura,M., Nakami,Y.,
Takayama,S., Endo,T., Saruwatari,T., Yagura,M., Yoshikawa,Y.,
Fujimoto,K., Oka,A., Chiku,S., Linsen,S.E., Giphart,M.J.,
Kulski,J.K., Fukazawa,T., Hashimoto,H., Kimura,M., Hoshina,Y.,
Suzuki,Y., Hotta,T., Mochida,J., Minezaki,T., Komai,K.,
Shiozawa,S., Taniguchi,A., Yamanaka,H., Kamatani,N., Gojobori,T.,
Bahram,S. and Inoko,H.
TITLE Whole genome association study of rheumatoid arthritis using 27 039
microsatellites
JOURNAL Hum. Mol. Genet. 14 (16), 2305-2321 (2005)
PUBMED 16000323
REFERENCE 2 (bases 1 to 109)
AUTHORS Tamiya,G., Makino,S., Fujimoto,K., Oka,A., Hayashi,H., Denda,A.,
Linsen,S.E., Ikuta,T., Shinya,M., Endo,T., Tomizawa,M., Tokubo,E.,
Sato,R., Takaki,A., Nagatsuka,Y., Watanabe,H., Adachi,S.,
Yanagino,Y., Nakano,S., Yamamoto,A., Yoshida,K., Okamoto,K.,
Makaguchi,D., Ishibashi,H., Yonekura,M., Takayama,S., Nakami,Y.,
Saruwatari,T., Brand,A., van Hiltten,J.A., van de Watering,L.M.,
Giphart,M.J., Bahram,S., Kulski,Y.J. and Inoko,H.
TITLE Direct Submision
JOURNAL Submitted (12-DEC-2003) Hidetoshi Inoko, Tokai University School of
Medicine, Department of Genetic Information, Bonseidai, Isehara,
Kanagawa 259-1193, Japan (E-mail:hinoko@is.icc.u-tokai.ac.jp,
Tel:81-463-93-1121, Fax:81-463-94-8884)
COMMENT Polymorphisms were confirmed by comparing with the pooled DNA
typing data of 88 Dutch population or 100 Australian. When there
was no significant difference between the Japanese and these
Caucasians, individual typing was performed to confirm
polymorphisms.
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/chromosome="10"
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DB 42 CTGAGTTTTCAGGCGCAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAG 101

QY 198 CT 199
DB 102 CT 103

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RESULT 4
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LOCUS      AX900201
DEFINITION Sequence 16064 from Patent EP1033401.
ACCESSION  AX900201
VERSION     AX900201.1 GI:40055115
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE     Expressed sequence tags and encoded human proteins
JOURNAL   Patent: EP 1033401-A 16064 06-SEP-2000;
          Genset (FR)
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Qy 156 CAGCTCGCAGTCGGGAGGAGGGGGGAGACAGCGGCTCTGGCCCC 207
Db 13 CAGCTCGAAATCGGAGCGGAACAGCGGGCTGGGAGCGGCGGCGCCCC 64

RESULT 5
BD035734
LOCUS      BD035734
DEFINITION Sequence tag and encoded human protein.
ACCESSION  BD035734
VERSION     BD035734.1 GI:22577476
KEYWORDS   JP 2001269182-A/11980.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 92)
AUTHORS   Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE     Sequence tag and encoded human protein
JOURNAL   Patent: JP 2001269182-A 11980 02-OCT-2001;
          GENSSET
COMMENT    OS Homo sapiens (human)
          PN JP 2001269182-A/11980
          PD 02-OCT-2001
          PF 24-FEB-2000 JP 2000118773
          PR 26-FEB-1999 US 60/122487
          PI JEAN BAPTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
          PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
          PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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Best Local Similarity 67.3%; Pred. No. 1.8e+04;

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RESULT 6
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ACCESSION  AR735995
VERSION     AR735995.1 GI:77429735
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 92)
AUTHORS   Edwards,J.-B.D.M., Duclert,A. and Giordano,J.-Y.
TITLE     Expressed sequence tags and encoded human proteins
JOURNAL   Patent: US 6783961-A 16064 31-AUG-2004;
          Genset S.A.;
          FRX;
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Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 156 CAGCTCGCAGTCGGGAGGAGGGGGGAGACAGCGGCTCTGGCCCC 207
Db 13 CAGCTCGAAATCGGAGCGGAACAGCGGGCTGGGAGCGGCGGCGCCCC 64

RESULT 7
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LOCUS      CQ471292
DEFINITION Sequence 3158 from Patent WO0160860.
ACCESSION  CQ471292
VERSION     CQ471292.1 GI:41436911
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE     Genes differentially expressed in human prostate cancer and their
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JOURNAL   Patent: WO 0160860-A 3158 23-AUG-2001;
          Millennium Predictive Medicine, Inc. (US)
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Qy 174 GGAGGGGGGGGAGAGAGCGGCTCTGGCCCCCTTAATTGTTACCTCGGCTCGTATTCT 233
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Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 156 CAGCTCGCAGTCGGGAGGAGGGGGGAGACAGCGGCTCTGGCCCC 207
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RESULT 6
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DEFINITION Sequence 16064 from patent US 6783961.
ACCESSION  AR735995
VERSION     AR735995.1 GI:77429735
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 92)
AUTHORS   Edwards,J.-B.D.M., Duclert,A. and Giordano,J.-Y.
TITLE     Expressed sequence tags and encoded human proteins
JOURNAL   Patent: US 6783961-A 16064 31-AUG-2004;
          Genset S.A.;
          FRX;
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SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE     Genes differentially expressed in human prostate cancer and their
          use
JOURNAL   Patent: WO 0160860-A 3158 23-AUG-2001;
          Millennium Predictive Medicine, Inc. (US)
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Db 62 CTCTCTCTCGCTAACGCC 80

RESULT 8  
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DEFINITION Sequence 12327 from Patent WO0160860.  
ACCESSION CQ480460  
VERSION CQ480460.1 GI:41446079  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;  
Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.B.  
TITLE Genes differentially expressed in human prostate cancer and their use  
JOURNAL Patent: WO 0160860-A 12327 23-AUG-2001;  
Millennium Predictive Medicine, Inc. (US)  
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Best Local Similarity 57.0%; Pred. No. 2.1e+04;  
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 174 GGAGGGGGGGGAGAGAGCGCTCTGCGCCCTTAATTCCTGCGGCTCGTATTGT 233  
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Qy 234 CTCTCTCTTCGCCACCTCC 252  
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RESULT 9  
AY751306  
LOCUS 119 bp mRNA linear PRI 19-MAY-2005  
DEFINITION Homo sapiens clone RW33 T cell receptor beta chain mRNA, partial cds.  
ACCESSION AY751306  
VERSION AY751306.1 GI:54111802  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;  
Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 119)  
AUTHORS Barcy, S., Huang, M.L., Corey, L. and Koelle, D.M.  
TITLE Longitudinal Analysis of Herpes Simplex Virus-Specific CD4+ Cell Clonotypes in Infected Tissues and Blood  
JOURNAL J. Infect. Dis. 191 (12), 2012-2021 (2005)  
PUBMED 15897986  
REFERENCE 2 (bases 1 to 119)  
AUTHORS Barcy, S.  
TITLE Direct Submission  
JOURNAL Submitted (14-SEP-2004) Laboratory Medicine, University of Washington, 1959 N.E. Pacific Street, Rosen Bldg, Room 154, Seattle, WA 98109, USA  
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Qy 37 CCCCAAGTTGGAAGGGCGCTTGTCTCTGTTTCTGGATGAGAGTCTCTGACTCCCTC 96  
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Qy 97 TGCACGGGCTGAGTTTCCGGCTCCAGGTT 126  
Db 69 TGGCTACACCTTCGGTTCGGGGACCAAGTT 98

RESULT 10  
AR431314  
LOCUS 96 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 1 from patent US 6651010.  
ACCESSION AR431314  
VERSION AR431314.1 GI:40193289  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 96)  
AUTHORS Han, K., Kim, D. and Kim, H.-J.  
TITLE Vector-based method for visualizing secondary structure of RNA molecules  
JOURNAL Patent: US 6651010-A 1 18-NOV-2003;  
INHA University Foundation; Incheon-si, KRX;  
FEATURES  
Location/Qualifiers  
1..96  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 9.6%; Score 24.2; DB 2; Length 96;  
Best Local Similarity 59.4%; Pred. No. 2.8e+04;  
Matches 41; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 32 GCGGTCCCAAGTTGGAAGGGCGCTTGTCTCTGTTTCTGGATGAGAGTCTCTGACT 91  
Db 10 GCGGCTGCAAGTCGAATTCGCTGCTCTCTGCTACGCGCTGCGTGGCTGACTG 69

Qy 92 CCCTCTGCC 100  
Db 70 GCTGCTGCC 78

RESULT 11  
AR477180/c  
LOCUS 78 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 145 from patent US 6696256.  
ACCESSION AR477180  
VERSION AR477180.1 GI:47234454  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 78)  
AUTHORS Li, X.  
TITLE Method, array and kit for detecting activated transcription factors by hybridization array

```

source
1. .78
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match          9.4%;   Score 23.8;   DB 2;   Length 78;
Best Local Similarity 59.7%;   Pred. No. 3.7e+04;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 109 AGTTTCGGCTCCAGGTTCCGTGTGCGCCTCAGGTTTCAGGGCCAGACAGCTCGCAGTCG 168
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 169 GGCAGGG 175
      |||||
Db 18 GTCAGAG 12

RESULT 14
AX899202/c
LOCUS AX899202 72 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 15065 from Patent EP1033401.
ACCESSION AX899202
VERSION AX899202.1 GI:40054115
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 15065 06-SEP-2000;
FEATURES
Genset (FR)
Location/Qualifiers
1. .72
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

source

Query Match          9.4%;   Score 23.6;   DB 2;   Length 72;
Best Local Similarity 69.6%;   Pred. No. 4.3e+04;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 128 GCGTGTGCGCCTCAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAG 173
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 GCGTGGGGGGGGGGATCGAGGCATCCAGCACAGAGCGGCCAG 13
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

ORIGIN

RESULT 15
BD034735/c
LOCUS BD034735 72 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD034735
VERSION BD034735.1 GI:22576477
KEYWORDS JP 2001269182-A/10981.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
1 (bases 1 to 72)
REFERENCE
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 10981 02-OCT-2001;
GENSET
COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/10981
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487

```

PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES  
 PI JORDAN  
 PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
 C12N5/10,  
 PC C12P21/02, C12P21/08, C12O1/68, G06F17/30, C12N15/00, C12N5/00, PC  
 G06F15/40  
 CC

FEATURES FH Key Location/Qualifiers.

source

1..72  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Query Match 9.4%; Score 23.6; DB 2; Length 72;  
 Best Local Similarity 69.6%; Pred. No. 4.3e+04;  
 Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 QY 128 GCGTGTGCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAG 173  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 58 GCGTGGGGCCCGGGGATCGAGGGCATCCACACAGAGCGGCCAG 13

Search completed: June 19, 2007, 14:28:18  
 Job time : 2233 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:10:19 ; Search time 372 Seconds  
(without alignments)  
5020.062 Million cell updates/sec

Title: US-10-604-726A-8797  
Perfect score: 252  
Sequence: 1 999ttatcgaactgagag.....tctctcttttcgcacactcc 252

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 6225436

Minimum DB seq length: 0  
Maximum DB seq length: 120

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_200701.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*  
15: Geneseqn2006s.\*  
16: Geneseqn2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	
1	25.6	10.2	115	6	ABQ76940 Polylinke	
C	25.2	10.0	96	15	AEG19874 Temp+ DNR	
3	25.2	10.0	96	15	AEG19878 Temp- DNR	
4	24.8	9.8	92	3	AAC11989 Human sec	
5	24.6	9.8	103	5	ABV03167 Human pro	
6	24.6	9.8	104	5	ABV12336 Human pro	
7	24.2	9.6	105	4	AH36160 Human col	
C	23.8	9.4	78	8	ABT17318 Transcrip	
C	23.6	9.4	72	3	AAC10990 Human sec	
10	23.6	9.4	97	4	AH68919 Human cer	
C	11	23.4	9.3	100	8	ACD69745 E. coli K
12	23.4	9.3	100	8	ACD76587 E. coli K	
13	23.4	9.3	100	13	ADR28210 Oligonuc	
14	23.4	9.3	100	13	ADR99734 Nucleic a	
C	15	23.2	9.2	59	Aaz89260 Human emb	
C	16	23.2	9.2	101	4	Aak44587 Human bon
C	17	23.2	9.2	101	4	Aak18659 Human bra

C	18	23.2	9.2	101	4	ABS44245
C	19	23.2	9.2	101	6	ABS18824
C	20	23.2	9.2	118	12	ACH88031
C	21	23	9.1	65	6	ABN28044 Rat epic
C	22	23	9.1	87	6	ABL75509 Corn tass
C	23	22.8	9.0	60	6	ABN43707 Human spl
C	24	22.8	9.0	88	13	ADQ91596 Template
C	25	22.8	9.0	117	9	ADA73750 Carcinoma
C	26	22.6	9.0	66	13	ABN15693 Human gen
C	27	22.6	9.0	66	13	ACN78783 Human GDM
C	28	22.4	8.9	119	3	AAC19710 Human sec
C	29	22.2	8.8	51	4	AAL33390 Human SNP
C	30	22.2	8.8	67	3	AAC11202 Human sec
C	31	22.2	8.8	88	13	ADR50936
C	32	22.2	8.8	88	13	ADR50937 Human mus
C	33	22.2	8.8	88	13	ADR50938 Human mus
C	34	22.2	8.8	102	3	AZ60564 A neublas
C	35	22.2	8.8	102	6	ABT11892 PCR produ
C	36	22.2	8.8	106	2	AAV46418 Ribosomal
C	37	22.2	8.8	115	3	AAC16203 Human sec
C	38	22.2	8.7	115	9	ACL25369 DNA clone
C	39	22	8.7	68	15	AEE99649 Mouse mir
C	40	22	8.7	89	14	ADX04314 Mouse pri
C	41	22	8.7	93	2	AQ97727 Toxoplasm
C	42	22	8.7	102	14	AEB50490 Human myo
C	43	22	8.7	113	4	ABA36569 Probe #15
C	44	21.8	8.7	61	3	AZ89261 Human emb
C	45	21.8	8.7	93	14	ACL68051 M. xanthu

# ALIGNMENTS

## RESULT 1

ABQ76940  
ID ABQ76940 standard; DNA; 115 BP.

XX ABQ76940;

XX 27-MAR-2003 (first entry)

XX Polylinker ScaI-Li-(BsgI-ScaI) DNA.

XX Murine; T cell receptor; TCR; hdm2; T cell response; alpha TCR; beta TCR;  
XX antigen-recognising sequence; ARS; fusion construct; cytostatic;  
XX apoptotic; tumour; leukaemia; immunisation; ds.

XX Synthetic.

XX DE10109854-A1.

XX 12-SEP-2002.

XX 01-MAR-2001; 2001DE-01009854.

XX 01-MAR-2001; 2001DE-01009854.

XX (STAN/) STANISLAWSKI T.

XX Theobalt M, Voss H, Stanislawski T;

XX WPI; 2002-714556/78.

XX P-PSDB; ABG73655.

XX New polypeptide of a murine alpha/beta T-cell receptor, useful for  
XX treating tumors and leukemia, induces specific lysis or apoptosis of cells  
XX expressing hdm2 protein.

XX Example 2; Fig 6; 52pp; German.

XX This invention describes a novel murine alphabeta T-cell receptor (TCR)  
XX that mediates a hdm2 protein-specific T cell response, a fusion protein  
XX (FP) that includes the TCR and nucleic acid encoding it, alpha or beta-



chains of a TCR that include the antigen-recognizing sequence (ARS) of an antibody specific for aa 81-88 of hdm2 (or its complex with HLA-A2-specific antibody) and a method for identifying hdm2-specific antigens. The TCR of the invention has cytostatic and apoptotic activity. The products of the invention are useful for treatment, prevention and diagnosis of hdm2-associated diseases, particularly tumours and leukemia, including use for passive or active immunisation. They can also be used to screen for therapeutic agents. This sequence encodes the polypeptide Sca1-Li-(B9g1-Sca1) fragment used in the construction of the fusion constructs described in the disclosure of the invention

Sequence 115 BP; 19 A; 33 C; 47 G; 16 T; 0 U; 0 Other;

	Query Match	10.2%	Score 25.6;	DB 6;	Length 115;
	Best Local Similarity	52.9%	Pred. No. 1.4e+03;		
	Matches	55;	Conservative	Mismatches 49;	Indels 0; Gaps 0;
Qy	106	CTGAGTTTCGGCTCCAGGTTCCGGTGTCCGCTTGAGGTCAGAGCTCCGAG	165		
Db	9	CTTCGGTCCCGGCACAGGCTCAGGTTGCGCGGAGGCAGCGCGCGGAGGACGCG	68		
Qy	166	TCGGGGAGGAGGCGCGGGGAGAGACAGAGCGGCTCTCGCCCCCTT	209		
Db	69	CGCGGAGGAGCGGTGCAGCAGAGTCTCGATCCTTGAGTACTT	112		

RESULT 2  
AEG19874/c  
ID AEG19874 standard; DNA; 96 BP.

XX	
AC	AGE19874;
XX	
DT	18-MAY-2006 (first entry)
XX	
DE	Temp+ DNA.
XX	
KW	ds; DNA amplification; ligase chain reaction; fluorescence;
KW	DNA detection; diagnosis; mutagenesis; DNA sequencing.
XX	
OS	Unidentified.

XX	US2006057611-A1.
PN	
XX	
XX	16-MAR-2006.
PD	
XX	
XX	30-JUN-2005; 2005US-00173902.
PF	
XX	
XX	30-JUN-2004; 2004US-0584665P.
PR	
XX	
XX	(APPL-) APPLERA CORP.
PA	

XX Kao HP, Lao KQ, Jones R;  
XX  
DR WPI: 2006-239070/25.

Quantitating target sequences for e.g. diagnosis, comprises exponentially amplifying a target to form exponential amplicons, and linearly amplifying exponential amplicons to form linear amplicons.

Example 2: SEQ ID NO 22: 34bp: English.

The present nucleic acid sequence was used in the current invention relating to quantitating target sequences by exponentially amplifying sequences in a reaction that terminates when a selected number of exponential amplicons are produced, linearly amplifying an exponential amplicon to produce linear amplicons in coupled reactions that produces a detectable signal proportional to a linear amplicon, and measuring fluorescence signals as a function of the amplification cycle number. The invention further relates to obtaining a cycle number (Ct) and a copy number of a nucleic acid amplification reaction by exponentially and linearly amplifying a target sequence in a coupled reaction under conditions in which the exponential amplification terminates before reaching a plateau and a reporter molecule generates a detectable signal

proportional to the number of linear stranded amplicons, measuring the detectable signal as a function of cycle number, and obtaining from it the  $C_e$  value of the amplification reaction. The detectable signal is produced by a reporter molecule, where the reporter molecule is a self-quenching fluorescence probe, peptide nucleic acid (PNA) probe or 5'-nuclease or flap hydrolyzable probe. The target sequence is amplified in a thermal cycling reaction comprising forward and reverse amplification primers, hydrolyzable probe and thermostable polymerase having 5'-3' nuclease activity, where the forward primer is in excess of the reverse primer by at least 50:1, the probe hybridizes to a target sequence 3' relative to the forward primer, where the conditions of the reaction are effective for the forward primer, probe, and target sequence to form a substrate for the nuclease activity and for the nuclease activity to hydrolyze the probe to generate the detectable signal. The melting temperatures ( $T_m$ ) of the forward primer, reverse primer and probe with the target sequence are 5 degrees C or less. The conditions terminate the exponential phase at or before the cycle number that the exponential phase is capable of producing a detectable signal. The method is useful for amplifying one or more target polynucleotide sequences of an unknown polymer accurately, sensitively and specifically with high throughput capacity using array based assays or by single-strand conformational analysis, and in diagnosis or testing. Log-linear amplification may be used to produce templates for nucleic acid sequencing or for use in mutagenesis and gene expression analysis.

Sequence 96 BP; 20 A; 18 C; 40 G; 18 T; 0 U; 0 Other;

Query Match	10.0%	Score 25.2	DB 15	Length 96
Best Local Similarity	60.0%	Pred. No. 1.7e+03		
Matches 42: Conservative	0	Mismatches 28	Indels 0	Gaps 0

69 TC TGGATGAGAGTCCTCTGCACTCCCTCTGCGCA CGGGCTGAGTTTCCGGCTCCAGGTTCC 128  
90 TCCAGCTCCGGAACCTGTGAAGACCTCAGCAACTCTGTATTTTCCGTGCACGGGTTCC 31  
ph

Qy 129 CGTGTGCCC 138  
|||  
Db 30 CGCTTCGCC 21

RESULT 3  
AEG19878  
ID AEG19878 standard; DNA; 96 BP.

AA AEG19878:

18-MAY-2006 (first entry)

DE Temp- DNA.

ds; DNA amplification; ligase chain reaction; fluorescence;  
kw DNA detection; diagnosis; mutagenesis; DNA sequencing.  
xx

XX Unidentified

XX  
PN  
IIS2006057611-A1XX  
16-MAR-2006

30-JUN-2005: 2005UIS-00173902.

30-JUN-2004: 2004IIS-0584665P-XX  
BBXX  
PA (APPT.-) APPT.ERA CORP.

XX  
BT  
KAO HP  
Lao KO  
Jones R.

XX  
DB WPT: 2006-239070/25

xx Quantitating target sequences for e.g. diagnosis, comprises exponentially  
 pr amplifying a target to form exponential amplicons, and linearly  
 pt amplifying a target to form linear amplicons.  
 pr amplifying exponential amplicons to form linear amplicons.

PS Example 2; SEQ ID NO 23; 34pp; English.

XX The present nucleic acid sequence was used in the current invention

CC relating to quantitating target sequences by exponentially amplifying

CC sequences in a reaction that terminates when a selected number of

CC exponential amplicons are produced, linearly amplifying an exponential

CC amplicon to produce linear amplicons in coupled reactions that produces a

CC detectable signal proportional to a linear amplicon, and measuring

CC fluorescence signals as a function of the amplification cycle number. The

CC invention further relates to obtaining a cycle number (C<sub>e</sub>) and a copy

CC number of a nucleic acid amplification reaction by exponentially and

CC linearly amplifying a target sequence in a coupled reaction under

CC conditions in which the exponential amplification terminates before

CC reaching a plateau and a reporter molecule generates a detectable signal

CC proportional to the number of linear stranded amplicons, measuring the

CC detectable signal as a function of cycle number, and obtaining from it

CC the C<sub>e</sub> value of the amplification reaction. The detectable signal is

CC produced by a reporter molecule, where the reporter molecule is a self-

CC quenching fluorescence probe, peptide nucleic acid (PNA) probe or 5'-

CC nuclease or flap hydrolyzable probe. The target sequence is amplified in

CC a thermal cycling reaction comprising forward and reverse amplification

CC primers, hydrolyzable probe and thermostable polymerase having 5'-3',

CC nuclease activity, where the forward primer is in excess of the reverse

CC primer by at least 50:1, the probe hybridizes to a target sequence 3'

CC relative to the forward primer, where the conditions of the reaction are

CC effective for the forward primer, probe, and target sequence to form a

CC substrate for the nuclease activity and for the nuclease activity to

CC hydrolyze the probe to generate the detectable signal. The melting

CC temperatures (T<sub>m</sub>) of the forward primer, reverse primer and probe with

CC the target sequence are 5 degrees C or less. The conditions terminate the

CC exponential phase at or before the cycle number that the exponential

CC phase is capable of producing a detectable signal. The method is useful

CC for amplifying one or more target polynucleotide sequences of an unknown

CC polymer accurately, sensitively and specifically with high throughput

CC capacity using array based assays or by single-strand conformational

CC analysis, and in diagnosis or testing. Log-linear amplification may be

CC used to produce templates for nucleic acid sequencing or for use in

CC mutagenesis and gene expression analysis. Note: The present sequence is

CC not shown in the patent but is a version of ABG19875 in the reverse (5'-

CC 3') orientation.

XX

SQ Sequence 96 BP; 18 A; 40 C; 18 G; 20 T; 0 U; 0 Other;

Query Match 10.0%; Score 25.2; DB 15; Length 96;

Best Local Similarity 60.0%; Pred. No. 1.7e+03;

Matches 42; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 69 TCTGGATGAGAGTCTCTGACTCCCTCTGCGACGGGCTGAGTTTCGGCTCCAGGTTG 128

DB 7 TCCAGCTCCCGAACCTCTGTGAGACCTCTGACCACTCTGTATTTTCGGTGACCGGTTCC 66

QY 129 CGTGTGCCCC 138

DB 67 CGCTTCGCC 76

RESULT 4

AAC11989

ID AAC11989 standard; cDNA; 92 BP.

XX

AC AAC11989;

XX

06-OCT-2000 (first entry)

XX

DE Human secreted protein 5' EST; SEQ ID NO: 16064.

XX

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KW gene therapy; chromosome mapping; ss.

KW

XX Homo sapiens.

OS

XX EP1033401-A2.

PN

XX

PD 06-SEP-2000.

XX

PF 21-FEB-2000; 2000EP-00200610.

XX

PR 26-FEB-1999; 99US-0122487P.

XX

PA (G8ST ) GENSET.

XX

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

DR

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

PS Claim 1; SEQ ID NO 16064; 71pp + Sequence Listing; English.

XX

CC The present sequence is one of a large number of 5' ESTs derived from

CC mRNAs encoding secreted proteins. No ORF has yet been conclusively

CC identified within the present sequence. The 5' ESTs were prepared from

CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST

CC sequences usually correspond mainly to the 3' untranslated region (UTR)

CC of the mRNA because they are often obtained from oligo-dT primed cDNA

CC libraries. Such ESTs are not well suited for isolating cDNA sequences

CC derived from the 5' ends of mRNAs and even in those cases where longer

CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'

CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used

CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in

CC diagnostic, forensic, gene therapy and chromosome mapping procedures.

CC They are used to obtain upstream regulatory sequences and to design

CC expression and secretion vectors

XX

SQ Sequence 92 BP; 19 A; 24 C; 44 G; 5 T; 0 U; 0 Other;

Query Match 9.8%; Score 24.8; DB 3; Length 92;

Best Local Similarity 67.3%; Pred. No. 2.2e+03;

Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 156 CAGTCTCGAGTCGGCGGAGGGGGGGGAGACGACGAGCGGCTCTGGCCCC 207

DB 13 CAGCTCGAATCGGAGCGGAAACAGCGGGGCTGGGAGCGGCGGCGCCCC 64

RESULT 5

ABV03167

ID ABV03167 standard; cDNA; 103 BP.

XX

AC ABV03167;

XX

13-SEP-2002 (first entry)

XX

XX Human prostate expression marker cDNA 3158.

DE

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW pharmacogenomic marker; gene; ss.

KW

XX Homo sapiens.

OS

XX WO200160860-A2.

PN

XX

23-AUG-2001.

XX

XX

20-FEB-2001; 2001WO-US005171.

XX

XX 17-FEB-2000; 2000US-0183319P.

PR 16-MAR-2000; 2000US-0189862P.

PR 25-MAY-2000; 2000US-0207454P.

PR 09-JUN-2000; 2000US-0211314P.

PR 18-JUL-2000; 2000US-0219007P.

PR 13-DEC-2000; 2000US-0255281P.

XX

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.



CC cancer antigens have cytostatic activity and can be used in gene therapy  
CC and vaccine production. N and P may be used in the prevention, diagnosis  
CC and treatment of diseases associated with inappropriate P expression. For  
CC example, N and P may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of P by expressing inactive proteins or to  
CC supplement the patients own production of P. Additionally, N may be used  
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids  
CC into a host cell and culturing the cell to express the proteins. N and P  
CC can be used in the prevention, diagnosis and treatment of colorectal  
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent  
CC sequences used in the exemplification of the present invention. N.B.  
CC Pages 666 to 682 and page 7033 of the sequence listing were missing at  
CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
CC to 1052, 7921 and 7922  
XX  
SQ Sequence 105 BP; 24 A; 36 C; 32 G; 8 T; 0 U; 5 Other;

Query Match 9.6%; Score 24.2; DB 4; Length 105;  
Best Local Similarity 53.7%; Pred. No. 3.4e+03;  
Matches 44; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 96 CTGCCAGGGCTCAGTTTCGGCTCCAGGTTCCGGTTCGGCTCCAGGTTGAGGTTGAGGCCAGA 155  
DB 24 CCGNACGCCCGCAGGNACCGGTCCGGAATCCGGTCCGACCACCGCNTTCNGCCAAA 83  
QY 156 CAGCTCGCAGTCGGGAGGGAG 177  
DB 84 CATGGCGGGCAGACGGGGG 105

RESULT 8  
ABT17318/c  
ID ABT17318 standard; DNA; 78 BP.  
XX  
AC ABT17318;  
XX  
XX  
DT 10-APR-2003 (first entry)  
XX  
DE Transcription factor-related array hybridisation probe - SEQ ID NO 145.  
XX  
KW Probe; ss; transcription factor-protein complex; transcription factor;  
XX drug screening; drug identification; array hybridisation.  
XX  
OS Unidentified.  
XX  
XX WO2002101351-A2.  
XX  
XX 19-DEC-2002.  
XX  
XX 30-MAY-2002; 2002WO-US017408.  
XX  
XX 08-JUN-2001; 2001US-00877243.  
XX 08-JUN-2001; 2001US-00877403.  
XX 08-JUN-2001; 2001US-00877705.  
XX 08-JUN-2001; 2001US-00877738.  
XX 05-SEP-2001; 2001US-00947274.  
XX  
XX (PANO-) PANOMICS INC.  
XX  
XX Li X;  
XX  
XX WPI; 2003-148829/14.  
XX  
XX  
PT Identifying transcription factor-protein complexes, by isolating  
PT transcription factor complexes from sample based on a specific type of  
PT factor, and identifying different proteins present in isolated complexes.  
XX  
XX  
PS Disclosure; Fig 6; 167pp; English.  
XX  
XX The invention comprises a method for identifying complexes between a  
XX transcription factor and another protein. The invention also comprises a  
XX method for isolating DNA probes which bind to activated transcription

CC factors. The methods of the invention are useful for identifying  
CC transcription factor-protein interactions. The methods of the invention  
CC are also useful for facilitating the screening and identification of new  
CC drugs, characterising their mechanism of action and screening for adverse  
CC side effects based on drug's impact expression. The present DNA sequence  
CC represents a probe used in the method of the invention  
XX  
SQ Sequence 78 BP; 15 A; 27 C; 15 G; 21 T; 0 U; 0 Other;

Query Match 9.4%; Score 23.8; DB 8; Length 78;  
Best Local Similarity 59.7%; Pred. No. 4.2e+03;  
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 109 AGTTTCGGCTCCAGGTTCCGGTTCGGCTCCAGGTTGAGGCCAGAGCTCGCAGTCG 168  
DB 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGAGCTAGCTTCAG 19  
QY 169 GGCAGGG 175  
DB 18 GTCAGAG 12

RESULT 9  
AAC10990/c  
ID AAC10990 standard; cDNA; 72 BP.  
XX  
XX AAC10990;  
XX AC  
XX 06-OCT-2000 (first entry)  
XX  
DE Human secreted protein 5' EST, SEQ ID NO: 15065.  
XX  
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
XX gene therapy; chromosome mapping; ss.  
XX  
XX Homo sapiens.  
XX  
XX EPI033401-A2.  
XX  
XX 06-SEP-2000.  
XX  
XX 21-FEB-2000; 2000EP-00200610.  
XX  
XX 26-FEB-1999; 99US-0122487P.  
XX  
XX (GEST ) GENSET.  
XX  
XX Dumas Milne Edwards J, Duclert A, Giordano J;  
XX WPI; 2000-500381/45.  
XX  
XX  
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
XX  
XX  
PS Claim 1; SEQ ID NO 15065; 71pp + Sequence Listing; English.  
XX  
XX The present sequence is one of a large number of 5' ESTs derived from  
XX mRNAs encoding secreted proteins. No ORF has yet been conclusively  
XX identified within the present sequence. The 5' ESTs were prepared from  
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
XX sequences usually correspond mainly to the 3' untranslated region (UTR)  
XX of the mRNA because they are often obtained from oligo-dT primed cDNA  
XX libraries. Such ESTs are not well suited for isolating cDNA sequences  
XX derived from the 5' ends of mRNAs and even in those cases where longer  
XX cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'  
XX ESTs are derived from mRNAs with intact 5' ends and can therefore be used  
XX to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in  
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.  
XX They are used to obtain upstream regulatory sequences and to design  
XX expression and secretion vectors  
XX  
XX Sequence 72 BP; 9 A; 33 C; 20 G; 10 T; 0 U; 0 Other;



XX E. coli K12 MG1655 biochip probe SEQ ID 7863.  
DE Biochip; gene expression; gut; diagnostic; detection; probe; ss.  
XX Escherichia coli.  
XX EPI260592-A1.  
XX 27-NOV-2002.  
XX 17-MAY-2001; 2001EP-00112179.  
XX 17-MAY-2001; 2001EP-00112179.  
XX (MWGB-) MWG-BIOTECH AG.  
XX Donner H, Drescher B, Huber A, Weber J;  
XX WPI; 2003-241155/24.  
XX Biochip containing probes complementary with open reading frames in  
PT Escherichia coli K12, useful for detecting gene expression and expression  
PT patterns.  
XX Claim 3; Page 1228; 2004pp; German.  
XX This invention describes a novel biochip comprising probe spots, each  
CC containing many identical probes. The probes are nucleotide sequences of  
CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at  
CC least one includes a segment of at least 20 bases identical with, or  
CC complementary to, a segment of an open reading frame (orf) of Escherichia  
CC coli K12. The biochip is used for specific detection of gene expression  
CC in K12 and for determining the gene expression pattern, e.g. for  
CC diagnostic determination of which E. coli strains are present in the gut,  
CC and to determine the effects of e.g. growth media on gene expression. The  
CC biochip provides as comprehensive as possible detection of the K12  
CC genome, with simultaneous analysis of many different genes with a single  
CC device, and comparison of gene expression between K12 and its mutants or  
CC other E. coli strains in a single experiment. Apart from qualitative and  
CC quantitative information about gene expression, it also allows  
CC measurements of population densities for the various strains. The use of  
CC synthetic oligonucleotides for preparation of probes allows free  
CC variation in probe length and ensures high purity (and thus selectivity,  
CC reactivity and reproducibility); also synthetic probes are generally  
CC shorter than probes prepared by polymerase chain reaction. AC68731 to  
CC ACD81540 represent oligonucleotide probes used with the biochip described  
CC in the invention  
XX  
SQ Sequence 100 BP; 13 A; 35 C; 29 G; 23 T; 0 U; 0 Other;  
Query Match 9.3%; Score 23.4; DB 8; Length 100;  
Best Local Similarity 63.2%; Pred. No. 5.8e+03;  
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 100 CACGGCTGAGTTCCGGCTCCAGGTTCGGCTGCGCCCTGAGGTTGAGGCCAGAC 156  
DB 43 CAGTCTGCGCGCTGCACCATGTCGACGTGCGCGCGGTTCTGCGCAGCC 99  
RESULT 13  
ID ADR28210  
XX ADR28210 standard; DNA; 100 BP.  
AC ADR28210.  
XX ADR28210.  
XX 04-NOV-2004 (first entry)  
DT  
XX Oligonucleotide Dmeter, SEQ ID 9.  
DE  
XX 2-amino-4-alkylthio-butylric acid; methionine synthase;  
KW cystathionine-gamma-synthase; acylhomoserine sulphydrylase; ss.  
XX

OS Synthetic.  
XX FR2851255-A1.  
FN 20-AUG-2004.  
XX  
XX 14-MAY-2003; 2003FR-00005768.  
XX 18-FEB-2003; 2003FR-00001924.  
PR (META-) METABOLIC EXPLORER.  
XX  
XX Chateau M, Gonzales B, Soucaille PNP;  
PI WPI; 2004-618123/60.  
XX  
DR New strains of microorganisms that produce 2-amino-4-alkylthio-butylric  
PT acid, useful for preparing L-methionine, from simple carbon source and a  
PT mercaptan or its salt, have modified methionine synthase activity.  
XX  
PS Example 1; SEQ ID NO 9; 68pp; French.  
XX  
CC The present invention relates to a novel strain (A) of a microorganism  
CC which produces a 2-amino-4-alkylthio-butylric acid (I) by metabolising a  
CC simple sugar and a thiol (III), or its salt, and has at least one gene  
CC encoding an enzyme with modified methionine synthase (MS) activity. (A)  
CC are specifically used for fermentative production of L-methionine, which  
CC is produced from a simple carbon source and alkylmercaptan, i.e.  
CC synthesis of L-Met is independent of synthesis of cysteine; the methyl  
CC mercaptan used is a toxic waste product from the petrochemical industry  
CC and synthesis of L-Met occurs in a single step from O-(acetyl or  
CC succinyl)-L-homoserine. The enzyme with modified MS activity is either  
CC cystathionine-gamma-synthase or an acylhomoserine sulphydrylase, and is  
CC modified so that the substrate is reacted with (II) rather than with L-  
CC cysteine, to result in preferential conversion of the substrate to (I) or  
CC homocysteine. The present sequence was used in an example from the  
CC invention.  
XX  
SQ Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;  
Query Match 9.3%; Score 23.4; DB 13; Length 100;  
Best Local Similarity 63.2%; Pred. No. 5.8e+03;  
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 100 CACGGCTGAGTTCCGGCTCCAGGTTCGGCTGCGCCCTGAGGTTGAGGCCAGAC 156  
DB 12 CAGTCTGCGCGCTGCACCATGTCGACGTGCGCGCGGTTCTGCGCAGCC 68  
RESULT 14  
ADR99734  
ID ADR99734 standard; DNA; 100 BP.  
XX  
AC ADR99734;  
XX  
DT 02-DEC-2004 (first entry)  
DE  
XX Nucleic acid Dmeter to generate evolved microorganisms.  
XX  
KW ss; microorganism evolution; metabolic pathway; metabolite;  
KW biotransformation; NADPH-dependent enzyme; nucleic acid metabolism;  
KW lipid metabolism; sugar metabolism.  
OS Unidentified.  
XX  
XX WO2004076659-A2.  
FN 10-SEP-2004.  
PD  
XX 17-FEB-2004; 2004WO-FR000354.  
XX  
XX 18-FEB-2003; 2003FR-00001924.  
PR 14-MAY-2003; 2003FR-00005768.  
PR

PR 14-MAY-2003; 2003FR-00005769.  
PR 06-NOV-2003; 2003FR-00013054.  
XX (META-) METABOLIC EXPLORER.  
XX Chateau M, Gonzalez B, Meynial-Salles I, Soucaille PNP, Zink O;  
PI WPI; 2004-653418/63.  
XX  
XX New evolved microorganisms with altered metabolic pathways, useful e.g.  
XX for production of amino acids, are selected as mutants able to grow on  
XX defined media.  
XX  
XX Disclosure; SEQ ID NO 1; 113pp; French.  
XX  
XX The invention relates to a method for preparing evolved microorganisms  
XX (A) with modified metabolic pathways comprising: (a) genetic modification  
XX of a microorganism to inhibit production or consumption of a metabolite  
XX when it is grown on a defined medium, thus affecting its ability to grow;  
XX (b) growing the modified organism in the defined medium so that evolution  
XX can occur, optionally with addition of a co-substrate to allow evolution;  
XX and (c) selecting as (A) cells able to grow on the medium, optionally in  
XX presence of co-substrate. The evolved microorganisms (A), or evolved  
XX proteins (I) expressed by them, are useful in biotransformation  
XX processes, especially those involving NADPH-dependent enzymes,  
XX particularly synthesis of amino acids (Met, Cys, Thr, Lys or Ile) but  
XX also synthesis of nucleic acids or lipids, and metabolism of sugars. (A)  
XX provide more efficient production of selected metabolites than parent  
XX strains. This sequence represents a nucleic acid molecule used in the  
XX method of the invention.  
XX  
XX Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;  
SQ  
Query Match 9.3%; Score 23.4; DB 13; Length 100;  
Best Local Similarity 63.2%; Pred. No. 5.8e+03;  
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
Oy 100 CACGGGCTGAGTTTCCGGCTCCAGGTCGCGTGTGCGCCCTGAGGTTTGAGGCCAGAC 156  
Db 12 CAGTTCTGCCCGCCCTGCACCAATGTCGCCAGTCCGCGCGGGTTCTGCGCCAGCC 68  
RESULT 15  
AAZ89260/C  
ID AAZ89260 standard; DNA; 59 BP.  
XX AC AAZ89260;  
XX  
XX 09-JUN-2000 (first entry)  
XX Human embryonic brain protein PCR primer #5.  
XX Human; brain; nerve degeneration; neurotropic; neuroprotective;  
XX anticonvulsant; antiparkinsonian; antidiabetic; treatment; infarction;  
XX parkinson's disease; Alzheimer's disease; Huntington's disease;  
XX muscular hypoplastic lateral sclerosis; diabetic neuropathy; PCR primer;  
XX ss.  
XX Homo sapiens.  
XX OS  
XX WO200007614-A1.  
XX  
XX 17-FEB-2000.  
XX  
XX 02-AUG-1999; 99WO-JP004171.  
XX  
XX 05-AUG-1998; 98JP-00221886.  
XX  
XX 05-FEB-1999; 99JP-00029164.  
XX  
XX (SAKA) OTSUKA PHARM CO LTD.  
XX  
XX Horie M, Hirano H, Kyushiki H, Mitsuoto Y, Mori A, Watanabe A;  
PI  
XX

DR WPI; 2000-205568/18.  
XX New protein isolated from human embryonic brain useful for treating nerve  
PT degeneration diseases e.g. Parkinson's diseases and Alzheimer's disease.  
XX  
XX Example 2; Page 62; 69pp; Japanese.  
XX  
XX This invention describes a novel human embryonic brain derived protein  
CC (I) which has neurotropic, neuroprotective, anticonvulsant,  
CC antiparkinsonian and antidiabetic activity. (I) is useful for treating  
CC nerve degeneration diseases e.g. Parkinson's disease, Alzheimer's  
CC disease, muscular hypoplastic lateral sclerosis, Huntington's disease,  
CC brain infarction, diabetic neuropathy and traumatic nerve degeneration.  
CC AAZ89256-289234 represent PCR primers used in the isolation and  
CC amplification of the human brain protein described in the method of the  
CC invention  
XX  
XX Sequence 59 BP; 9 A; 23 C; 14 G; 13 T; 0 U; 0 Other;  
SQ  
Query Match 9.2%; Score 23.2; DB 3; Length 59;  
Best Local Similarity 65.4%; Pred. No. 5.8e+03;  
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
Oy 159 CTCGACGTCGGGCGGAGGGGGGGGAGAGAGAGCGGCTCTGCGCCCTTA 210  
Db 52 CTGGCAGTCGCTCAGGGAGGTGCGGAAAGAGCAGCAGCTTAACCGGGCGGCA 1  
Search completed: June 19, 2007, 13:36:55  
Job time : 376 secs

```

RESULT 2
US-09-210-305C-1
; Sequence 1, Application US/09210305C
; Patent No. 6651010
; GENERAL INFORMATION:
; APPLICANT: Inha University Foundation
; TITLE OF INVENTION: A vector-based method for
; visualizing secondary structure of RNA molecules
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BACHMAN & LAPOINTE, P.C.
; STREET: Suite 1201, 900 Chapel Street
; CITY: New Haven
; STATE: Connecticut
;

```



COUNTRY: U.S.A.  
 ZIP: 06510-2802  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
 COMPUTER: IBM  
 OPERATING SYSTEM: WINDOWS 95/98  
 SOFTWARE: MS WORD  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/210.305C  
 FILING DATE: 11-Dec-1998  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: oligonucleotide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-210-305C-1

Query Match 9.6%; Score 24.2; DB 3; Length 96;  
 Best Local Similarity 43.5%; Pred. No. 5.6e+02;  
 Matches 30; Conservative 11; Mismatches 28; Indels 0; Gaps 0;  
 QY 32 GGCCTCCCAAGTTGGAAGGCGCTTTCCTCTCTGTTTCTGATGCAGAGTCCTCTGACT 91  
 Db 10 GCGCCUGCAAGCGAAUUGCGUGUCUAGCGUAGCGUUGGUGGACUGGCU 69  
 QY 92 CCCTCTGCC 100  
 Db 70 GCUGCUGCC 78

RESULT 3  
 US-09-877-243A-145/c  
 ; Sequence 145, Application US/09877243A  
 ; Patent No. 6696256  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Jason  
 ; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED  
 ; FILE REFERENCE: 26757-702  
 ; CURRENT APPLICATION NUMBER: US/09/877,243A  
 ; CURRENT FILING DATE: 2001-08-16  
 ; NUMBER OF SEQ ID NOS: 162  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 145  
 ; LENGTH: 78  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hybridization probe MP74  
 US-09-877-243A-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;  
 Best Local Similarity 59.7%; Pred. No. 7e+02;  
 Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
 QY 109 AGTTTCGGCTCCAGGTTGCGGTGTCGCCCTGAGTTTGTAGGCCAGACAGCTCGCAGTCG 168  
 Db 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19  
 QY 169 GGCAGGG 175  
 Db 18 GTCAGAG 12

RESULT 4  
 US-09-877-705A-145/c  
 ; Sequence 145, Application US/09877705A  
 ; Patent No. 6821737  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Jason

; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPTION  
 ; TITLE OF INVENTION: FACTOR ACTIVITY  
 ; FILE REFERENCE: 26757-704  
 ; CURRENT APPLICATION NUMBER: US/09/877,705A  
 ; CURRENT FILING DATE: 2001-08-16  
 ; NUMBER OF SEQ ID NOS: 162  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 145  
 ; LENGTH: 78  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hybridization probe MP74  
 US-09-877-705A-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;  
 Best Local Similarity 59.7%; Pred. No. 7e+02;  
 Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
 QY 109 AGTTTCGGCTCCAGGTTGCGGTGTCGCCCTGAGTTTGTAGGCCAGACAGCTCGCAGTCG 168  
 Db 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19  
 QY 169 GGCAGGG 175  
 Db 18 GTCAGAG 12

RESULT 5  
 US-09-877-738C-145/c  
 ; Sequence 145, Application US/09877738C  
 ; Patent No. 6924113  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Jason  
 ; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED  
 ; FILE REFERENCE: 26757-701  
 ; CURRENT APPLICATION NUMBER: US/09/877,738C  
 ; CURRENT FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 162  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 145  
 ; LENGTH: 78  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hybridization probe MP74  
 US-09-877-738C-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;  
 Best Local Similarity 59.7%; Pred. No. 7e+02;  
 Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
 QY 109 AGTTTCGGCTCCAGGTTGCGGTGTCGCCCTGAGTTTGTAGGCCAGACAGCTCGCAGTCG 168  
 Db 78 AGCTTCAGGTCAGAGGTCAGAGAGTAGCTTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAG 19  
 QY 169 GGCAGGG 175  
 Db 18 GTCAGAG 12

RESULT 6  
 US-09-513-999C-15065/c  
 ; Sequence 15065, Application US/09513999C  
 ; Patent No. 6783961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Duclert, A.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; Patent No. 6783961  
 ; FILE REFERENCE: 59.US2.REG

```

; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 15065
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-513-999C-15065

```

Query Match	9.48;	Score 23.6;	DB 3;	Length 72;
Best Local Similarity	69.6;	Pred. No. 7.8e+02;		
Matches 32;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;
QY	128	GCCTGTGCGCCTGAGTGTGAGGCCACACAGCTCGAGTCGGGCAG	173	
Db	58	GCCTGGGGGCGCGGGGATCGAGGCGATCCAGACAGAGGGCGGCAG	13	

RESULT 7  
US-09-866-108A-15685/c

```

; Sequence 15685: Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSION
; FILE REFERENCE: AEOICA-7
; CURRENT APPLICATION NUMBER: US/09/866,111
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: AEOICA Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 15685
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-15685

```

Query Match 9.0%; Score 22.6; DB 3; Length 66;  
Best Local Similarity 64.2%; Pred. No. 1.5e+03;  
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
QY 86 CTGACTCCCTCTCCACGGGCTCAGTTTCGGGTCCAGGTTCCGGTCCGCC 138

```

Db      62  CTGTGCCCCACAGCACCGCCCTTTCTTTTCAGATCCAGGGTCTCCAGGAGCTC 10
;
RESULT 8
; US-09-513-999C-23785
; Sequence 23785, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Prote
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 23785
; .LENGTH: 119
; .TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-23785

```

	Query Match	8.9%	Score 22.4;	DB 3;	Length 119;
	Best Local Similarity	53.4%;	Pred. No. 2.1e+03;		
	Matches 47;	Conservative 0;	Mismatches 41;	Indels 0;	Gaps 0;
Qy	42	AGTTGGAGGCGCTTGGCTCTGTTTTCTGGATGAGAGTCTCTGACTCCCTCTGGCA	101		
Db	1	ACTTTGAACGTCTTTCTCTCTCTTTTGGCAGGAGTCTCATGCTGATATTTAGA	60		
Qy	102	CGGGCTGAGTTTCCGGCTCCAGTTCCG	129		
Db	61	CATGATCAGCTTTGTGCAAAAGGGAGC	88		

```

RESULT 9
US-09-513-999C-15277
; Sequence 15277, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 15277
; LENGTH: 67
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-15277

```

	Query Match	8.8%	Score 22.2;	DB 3;	Length 67;
	Best Local Similarity	64.7%;	Pred. No. 2.1e+03;		
	Matches 33;	Conservative	0;	Mismatches 18;	Indels 0;
	Gaps	0;			
Qy	156	CAGCTCGCAGTCCGGCAGGGAGGGCGGGGAGAGACGAGCGGTCTGTGGCCC	206		
Db	13	CCSCGCACTGTTCCGCGCGGAGAGCGCGGGGCCGAGAGCGTCACTCGCCCC	63		

RESULT 10  
US-09-347-613C-13/c

```
; Sequence 13, Application US/09347613C
; Patent No. 6593133
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
; APPLICANT: Hansen, Claus
; TITLE OF INVENTION: No. 6593133el Neurotrophic Factors
; FILE REFERENCE: NeuroSearch 19313-001
; CURRENT APPLICATION NUMBER: US/09/347,613C
; CURRENT FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-347-613C-13

Query Match      8.8%; Score 22.2; DB 3; Length 102;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 149 GGCAGACAGCTCCAGTCGGGAGGAGGCGGGGAGAGACGAGCGGCTCTGGCCCC 207
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Db 74 GGCAGCAGGCTGCTGACGGCGCGGAGCGCGGGGGGCTCGCAGGCGCCCGGGGCC 16

RESULT 11
US-09-662-183A-13/c
; Sequence 13, Application US/09662183A
; Patent No. 6734284
; GENERAL INFORMATION:
; APPLICANT: Johansen, Teit E.
; APPLICANT: Blom, Nikolaj
; APPLICANT: Hansen, Claus
; TITLE OF INVENTION: No. 6734284el Neurotrophic Factors
; FILE REFERENCE: 19313-001 DIV
; CURRENT APPLICATION NUMBER: US/09/662,183A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: DANISH 1998 00904
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: USSN 60/092,229
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: DANISH 1998 01048
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: USSN 60/097,774
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: DANISH 1998 01260
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: USSN 60/103,908
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: DANISH 1998 01265
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 09/347,613
; PRIOR FILING DATE: 2000-07-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 102
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-662-183A-13

Query Match      8.8%; Score 22.2; DB 3; Length 102;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 149 GGCAGACAGCTCCAGTCGGGAGGAGGCGGGGAGAGACGAGCGGCTCTGGCCCC 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 GGCAGCAGGCTGCTGACGGCGCGGAGCGCGGGGGGCTCGCAGGCGCCCGGGGCC 16

RESULT 12
US-09-367-927A-1/c
; Sequence 1, Application US/09367927A
; Patent No. 6300126
; GENERAL INFORMATION:
; APPLICANT: GRUMMT, INGRID
; APPLICANT: RAINWEG, MITTLERER
; APPLICANT: GRUMMT, FRIEDERICK
; APPLICANT: VAN DER VOGELWEIDE STRASSE, WALTHER
; TITLE OF INVENTION: EXPRESSION VECTOR FOR THE PERMANENT
; TITLE OF INVENTION: EXPRESSION OF FOREIGN DNA
; FILE REFERENCE: 35280043US00
; CURRENT APPLICATION NUMBER: US/09/367,927A
; CURRENT FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 113
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-367-927A-1

Query Match      8.8%; Score 22.2; DB 3; Length 113;
Best Local Similarity 64.7%; Pred. No. 2.4e+03;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 147 GAGCGCACAGCTCGCAGTCGGGAGGAGGCGGGGAGAGACGAGCGG 197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 GTGGCCCCCGCGCTCCGCGCGGGGGGGGGGGGGGGGACACTTTCGG 16

RESULT 13
US-09-513-999C-20278/c
; Sequence 20278, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 20278
; LENGTH: 115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-20278

Query Match      8.8%; Score 22.2; DB 3; Length 115;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 169 GGCAGGAGGCGGGGAGAGACGAGCGGCTCTGGCCCCCTTAATTGACTTCGGGCTCG 227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 63 GGGTGGGGGGCCCGGAGAGACAGCACCTCGAGCCCGAGATTGTTTTCGCTTTCG 5

RESULT 14

US-07-964-624D-57/c  
; Sequence 57, Application US/07964624D  
; Patent No. 5496938  
; GENERAL INFORMATION:  
; APPLICANT: GOLD, LARRY M.  
; APPLICANT: TUERK, CRAIG  
; TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC  
; TITLE OF INVENTION: ACIDS ON THE BASIS OF  
; TITLE OF INVENTION: STRUCTURE  
; NUMBER OF SEQUENCES: 83  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/964,624D  
; FILING DATE: 21-OCTOBER-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/714,131  
; FILING DATE: 10-JUNE-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/536,428  
; FILING DATE: 11-JUNE-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: NEX05  
; TELEPHONE: (303) 793-3333  
; TELEFAX: (303) 793-3433  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 86 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-964-624D-57

Query Match 8.7%; Score 21.8; DB 2; Length 86;  
Best Local Similarity 56.2%; Pred. No. 3e+03;  
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 84 CTCGTACTCCCTCTGCGAGGCTGAGTTTCGGCTCCAGGTTCCGCTGTCGCGCTGAGG 143

Db 86 CCGGATCTCTTTTACCTCTGTGTGAGCTCCAGAGTCCACTATCGTGTTCGATGGAG 27

Qy 144 TTTGAGGCCAGAC 156

Db 26 TTGTCGGAAGGC 14

RESULT 15

US-08-442-062-57/c  
; Sequence 57, Application US/08442062  
; Patent No. 5595877  
; GENERAL INFORMATION:  
; APPLICANT: GOLD, LARRY M.  
; APPLICANT: TUERK, CRAIG  
; TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC  
; TITLE OF INVENTION: ACIDS ON THE BASIS OF

TITLE OF INVENTION: STRUCTURE  
; NUMBER OF SEQUENCES: 83  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/442,062  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/964,624  
; FILING DATE: 21-OCTOBER-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/714,131  
; FILING DATE: 10-JUNE-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/536,428  
; FILING DATE: 11-JUNE-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: NEX05/D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 793-3333  
; TELEFAX: (303) 793-3433  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 86 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-442-062-57

Query Match 8.7%; Score 21.8; DB 2; Length 86;  
Best Local Similarity 56.2%; Pred. No. 3e+03;  
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 84 CTCGTACTCCCTCTGCGAGGCTGAGTTTCGGCTCCAGGTTCCGCTGTCGCGCTGAGG 143

Db 86 CCGGATCTCTTTTACCTCTGTGTGAGCTCCAGAGTCCACTATCGTGTTCGATGGAG 27

Qy 144 TTTGAGGCCAGAC 156

Db 26 TTGTCGGAAGGC 14

Search completed: June 19, 2007, 13:59:35  
Job time : 424 secs

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:37:11 ; Search time 3937 Seconds  
(without alignments)  
786.509 Million cell updates/sec

Title: US-10-604-726A-8797  
Perfect score: 252  
Sequence: 1 999ttatctgcaactgagag.....tctctcttctgccaactcc 252

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 1892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24482366

Minimum DB seq length: 0  
Maximum DB seq length: 120

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA\_Main:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
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- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27	10.7	67	11	US-10-310-914A-16611
C 2	25.2	10.0	96	16	US-11-173-902-22
C 3	25.2	10.0	109	9	US-10-674-124A-16551
C 4	24.6	9.8	103	9	US-10-357-930-3158
C 5	24.6	9.8	104	9	US-10-357-930-12327
C 6	24.2	9.6	105	6	US-10-106-698-3252
C 7	24	9.5	93	11	US-10-310-914A-17067
C 8	23.8	9.4	78	3	US-09-877-705A-145
C 9	23.8	9.4	78	3	US-09-947-274-145
C 10	23.8	9.4	78	3	US-09-877-738A-145
C 11	23.8	9.4	78	4	US-09-877-403A-145
C 12	23.8	9.4	78	8	US-10-779-595-145
C 13	23.4	9.3	100	10	US-10-781-499-1
C 14	23.4	9.3	120	3	US-09-796-692-6323
C 15	23.4	9.3	120	6	US-10-040-862-6323
C 16	23.4	9.3	120	7	US-10-057-475B-6323
C 17	23.4	9.3	120	7	US-10-154-884B-6323

18	23.4	9.3	120	9	US-10-764-324-6323	Sequence 6323, Ap
C 19	23.2	9.2	101	3	US-09-864-761-27544	Sequence 27544, A
C 20	23.2	9.2	118	7	US-10-029-386-21226	Sequence 21226, A
C 21	23	9.1	65	3	US-09-908-975-792	Sequence 792, App
C 22	23	9.1	87	3	US-09-294-093B-4883	Sequence 4883, App
C 23	22.8	9.0	60	3	US-09-908-975-16455	Sequence 16455, A
C 24	22.6	9.0	66	3	US-09-866-108-15685	Sequence 15685, A
C 25	22.6	9.0	66	8	US-10-723-361-15685	Sequence 15685, A
C 26	22.4	8.9	116	9	US-10-425-115-142012	Sequence 142012, App
C 27	22.2	8.8	102	3	US-09-804-615-13	Sequence 13, Appl
C 28	22.2	8.8	102	8	US-10-661-984A-13	Sequence 13, Appl
C 29	22.2	8.8	102	9	US-10-806-793-13	Sequence 387, App
C 30	22	8.7	68	10	US-10-490-955-387	Sequence 387, App
C 31	22	8.7	68	11	US-10-310-914A-2865	Sequence 2865, Ap
C 32	22	8.7	68	11	US-10-310-914A-3692	Sequence 3692, Ap
C 33	22	8.7	89	10	US-10-909-125-1425	Sequence 1425, Ap
C 34	22	8.7	99	11	US-10-310-914A-817	Sequence 817, App
C 35	22	8.7	104	8	US-10-242-535A-9222	Sequence 9222, Ap
C 36	22	8.7	104	8	US-10-085-783A-9222	Sequence 9222, Ap
C 37	22	8.7	113	3	US-09-864-761-21889	Sequence 21889, A
C 38	22	8.7	116	11	US-10-310-914A-12025	Sequence 12025, A
C 39	21.8	8.7	63	11	US-10-310-914A-20336	Sequence 20336, A
C 40	21.8	8.7	86	6	US-10-040-497-57	Sequence 57, Appl
C 41	21.8	8.7	86	9	US-10-818-954-57	Sequence 57, Appl
C 42	21.8	8.7	96	3	US-09-918-063-32	Sequence 32, Appl
C 43	21.8	8.7	96	3	US-09-918-063-34	Sequence 34, Appl
C 44	21.8	8.7	111	3	US-09-864-761-23937	Sequence 23937, A
C 45	21.8	8.7	113	3	US-09-933-797-725	Sequence 725, App

## ALIGNMENTS

### RESULT 1

US-10-310-914A-16611/c  
; Sequence 16611, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiller, Kruzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310.914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 16611

; LENGTH: 67

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-16611

Query Match 10.7%; Score 27; DB 11; Length 67;  
Best Local Similarity 85.7%; Pred. No. 2e+02;  
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	174	GGAGGGGGGGGAGAGAGAGCGGCTCTGGGCCCT	208
Db	67	GGAGGGTGGGGAGAGAGAGCCCTGGGCCCT	33

### RESULT 2

US-11-173-902-22/c  
; Sequence 22, Application US/11173902  
; Publication No. US20060057611A1  
; GENERAL INFORMATION:  
; APPLICANT: KAO, H. PIN  
; APPLICANT: LAO, KAI QIN  
; APPLICANT: JONES, ROBERT  
; TITLE OF INVENTION: LOG-LINEAR AMPLIFICATION  
; FILE REFERENCE: 375461-021US  
; CURRENT APPLICATION NUMBER: US/11/173.902



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RESULT 6
US-10-106-698-3252
/ Sequence 3252, Application US/10106698
/ Publication No. US2003010960A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Colon and Colon Cancer
/ FILE REFERENCE: PA00591
/ CURRENT APPLICATION NUMBER: US/10/106,698
/ CURRENT FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: PCT/US00/26524
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: US 60/157,137
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: US 60/163,280
/ PRIOR FILING DATE: 1999-11-03
/ NUMBER OF SEQ ID NOS: 8564
/ SOFTWARE: PatentIn Ver. 3.0
/ SEQ ID NO 3252
/ LENGTH: 105
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (28)..(28)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (40)..(40)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (53)..(53)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (72)..(72)
/ OTHER INFORMATION: n equals a,t,g, or c
/ NAME/KEY: misc_feature
/ LOCATION: (77)..(77)
/ OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-3252

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	Query Match :	9.4%	Score 23.8;	DB 3;	Length 78;
	Best Local Similarity	59.7%;	Pred. No. 2.1e+03;		
	Matches	40;	Conservative	0;	Mismatches 27; Indels 0; Gaps 0;
Qy	109	AGTTTCGGGCTCCAGGTTTCGGGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG	168		
Db	78	AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGTCAGAGGTCAGAGAGCTAGCTTCAG	19		
Qy	169	GGCAGGG	175		

Db 18 GTCAGAG 12

## RESULT 9

US-09-947-274-145/c

; Sequence 145, Application US/09947274

; Publication No. US20030017499A1

; GENERAL INFORMATION:

; APPLICANT: Li, Xianqiang

; TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS

; FILE REFERENCE: 26757-705

; CURRENT APPLICATION NUMBER: US 09/947,274

; CURRENT FILING DATE: 2001-09-05

; PRIOR APPLICATION NUMBER: US 09/877,738

; PRIOR FILING DATE: 2000-06-08

; PRIOR APPLICATION NUMBER: US 09/877,243

; PRIOR FILING DATE: 2000-06-08

; PRIOR APPLICATION NUMBER: US 09/877,403

; PRIOR FILING DATE: 2000-06-08

; PRIOR APPLICATION NUMBER: US 09/877,705

; PRIOR FILING DATE: 2000-06-08

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 145

; LENGTH: 78

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74

US-09-947-274-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;

Best Local Similarity 59.7%; Pred. No. 2.1e+03;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 109 AGTTTCGGCTCCAGGTTCCGGTGTGCGCCCTGAGGTTTGAGGCCACAGAGCTCGAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAG 19

Qy 169 GGCAGGG 175

Db 18 GTCAGAG 12

## RESULT 10

US-09-877-738A-145/c

; Sequence 145, Application US/0987738A

; Publication No. US20030022173A1

; GENERAL INFORMATION:

; APPLICANT: Li, Jason

; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED

; FILE REFERENCE: 26757-701

; CURRENT APPLICATION NUMBER: US/09/877,738A

; CURRENT FILING DATE: 2001-06-01

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 145

; LENGTH: 78

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74

US-09-877-738A-145

Query Match 9.4%; Score 23.8; DB 3; Length 78;

Best Local Similarity 59.7%; Pred. No. 2.1e+03;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 109 AGTTTCGGCTCCAGGTTCCGGTGTGCGCCCTGAGGTTTGAGGCCACAGAGCTCGAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAG 19

Qy 169 GGCAGGG 175

Db 18 GTCAGAG 12

## RESULT 11

US-09-877-403A-145/c

; Sequence 145, Application US/09877403A

; Publication No. US20040214166A1

; GENERAL INFORMATION:

; APPLICANT: Li, Jason

; TITLE OF INVENTION: METHOD FOR IDENTIFYING A DISEASE STATE BASED ON A DETECTED MIXTURE

; FILE REFERENCE: 26757-703

; CURRENT APPLICATION NUMBER: US/09/877,403A

; CURRENT FILING DATE: 2001-08-10

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 145

; LENGTH: 78

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74

US-09-877-403A-145

Query Match 9.4%; Score 23.8; DB 4; Length 78;

Best Local Similarity 59.7%; Pred. No. 2.1e+03;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 109 AGTTTCGGCTCCAGGTTCCGGTGTGCGCCCTGAGGTTTGAGGCCACAGAGCTCGAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAG 19

Qy 169 GGCAGGG 175

Db 18 GTCAGAG 12

## RESULT 12

US-10-779-595-145/c

; Sequence 145, Application US/10779595

; Publication No. US20040132090A1

; GENERAL INFORMATION:

; APPLICANT: Li, Xianqiang

; TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOR

; FILE REFERENCE: 26757-702.301

; CURRENT APPLICATION NUMBER: US/10/779,595

; CURRENT FILING DATE: 2004-02-13

; PRIOR APPLICATION NUMBER: 09/877,243

; PRIOR FILING DATE: 2001-06-08

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 145

; LENGTH: 78

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Hybridization probe MP74

US-10-779-595-145

Query Match 9.4%; Score 23.8; DB 8; Length 78;

Best Local Similarity 59.7%; Pred. No. 2.1e+03;

Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 109 AGTTTCGGCTCCAGGTTCCGGTGTGCGCCCTGAGGTTTGAGGCCACAGAGCTCGAGTCG 168

Db 78 AGCTTCAGGTCAGAGGTCAGAGAGCTAGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAG 19

Qy 169 GGCAGGG 175

Db 18 GTCAGAG 12



RESULT 13  
US-10-781-499-1  
; Sequence 1, Application US/10781499  
; Publication No. US20050054060A1  
; GENERAL INFORMATION:  
; APPLICANT: Metabolic Explorer  
; TITLE OF INVENTION: Method for the preparation of an evolved microorganism for the ca  
; FILE OF INVENTION: or modification of metabolic pathways  
; FILE REFERENCE: D20701/ 345774  
; CURRENT APPLICATION NUMBER: US/10781.499  
; CURRENT FILING DATE: 2004-02-18  
; PRIOR APPLICATION NUMBER: FR 0301924  
; PRIOR FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: FR 0305768  
; PRIOR FILING DATE: 2003-05-14  
; PRIOR APPLICATION NUMBER: FR 0305769  
; PRIOR FILING DATE: 2003-05-14  
; PRIOR APPLICATION NUMBER: FR 0313054  
; PRIOR FILING DATE: 2003-11-06  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 100  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Dmeter  
US-10-781-499-1

Query Match 9.3%; Score 23.4; DB 10; Length 100;  
Best Local Similarity 63.2%; Pred. No. 3e+03;  
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
Qy 100 CAGCGGTGAGTTCCGGCTCCAGGTTCCGCTGTCGCCCTGAGCTTTGAGGCCAGAC 156  
Db 12 CAAGTTCTGCCGCCCTGCACCATGTTCCGACGTCGCCGCGGCTTTCTGCCACGCC 68

RESULT 14  
US-09-796-692-6323  
; Sequence 6323, Application US/09796692  
; Publication No. US20020198362A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
; FILE OF INVENTION: HEMATOLOGICAL MALIGNANCIES  
; FILE REFERENCE: 2077.001200  
; CURRENT APPLICATION NUMBER: US/09796.692  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6323  
; LENGTH: 120  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-040-862-6323

; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 9597  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6323  
; LENGTH: 120  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-796-692-6323

Query Match 9.3%; Score 23.4; DB 3; Length 120;  
Best Local Similarity 60.0%; Pred. No. 3e+03;  
Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
Qy 141 AGGTTTGAGGCCACAGACATCGCAGTCGGGCGGAGGCGGCGGAGAGACGAGCGGCTC 200  
Db 53 AGGTTTGATGCAAGATGCTCTGGGAAGTGCACCGCAGATATGGGGGGGAGAAAAGCTGCTC 112  
Qy 201 TGGCC 205  
Db 113 AGACC 117

RESULT 15  
US-10-040-862-6323  
; Sequence 6323, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/040.862  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6323  
; LENGTH: 120  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-040-862-6323

Query Match 9.3%; Score 23.4; DB 6; Length 120;  
Best Local Similarity 60.0%; Pred. No. 3e+03;  
Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 141 AGGTTTGAGCCACAGACAGCTCGCAGTCGGCAGGGGCGGGGAGAGACGAGCGGCTC 200  
Db 53 AGGTTTGATGCAAGATGCTCTGGGAAGTCACGCAGATATGGGGGAGAGAAAGCTGCTC 112  
QY 201 TGGCC 205  
Db 113 AGACC 117

Search completed: June 19, 2007, 18:07:52  
Job time : 3939 secs

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:30:48 ; Search time 12307 seconds  
(without alignments)  
1270.361 Million cell updates/sec

Title: US-10-604-726A-8797  
Perfect score: 252  
Sequence: 1 ggggtatctgcaactgagag.....tctctcttcctgcacctcc 252

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 1909528

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: gb\_est1.\*

2: gb\_est3.\*

3: gb\_est4.\*

4: gb\_est5.\*

5: gb\_est6.\*

6: gb\_est7.\*

7: gb\_est8.\*

8: gb\_est9.\*

9: gb\_est10.\*

10: gb\_est11.\*

11: gb\_est12.\*

12: gb\_est13.\*

13: gb\_est14.\*

14: gb\_est15.\*

15: gb\_gss1.\*

16: gb\_gss2.\*

17: gb\_gss3.\*

18: gb\_gss4.\*

19: gb\_gss5.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	11.5	100	15	AZ769498
2	28.6	11.3	103	12	EC491510
3	28	11.1	97	12	EC465112
4	27.6	11.0	103	17	CG574657
5	27	10.7	110	11	EE366986
6	26.2	10.4	82	17	CG535738
7	25.8	10.2	93	11	EC566335
8	25.8	10.2	110	9	CK014560
9	25.8	10.2	110	17	CL952591
10	25.8	10.2	111	12	EB652145
11	25.8	10.2	113	12	EC536793
12	25.6	10.2	99	7	AV841732
13	25.6	10.2	103	18	DU408432
14	25.6	10.2	117	17	CG255380

C 15	25.2	10.0	103	7	AW800261
C 16	25.2	10.0	103	12	EC523717
C 17	25.2	10.0	112	5	BY857392
C 18	25	9.9	100	12	DV900899
C 19	25	9.9	108	15	AZ697609
C 20	24.8	9.8	89	2	BG718505
C 21	24.8	9.8	116	16	BZ836170
C 22	24.8	9.8	120	19	CNS02660
C 23	24.6	9.8	107	8	CB219192
C 24	24.6	9.8	109	11	EC547122
C 25	24.6	9.8	119	16	BZ987003
C 26	24.4	9.7	95	2	BF724320
C 27	24.4	9.7	109	13	DV552589
C 28	24.4	9.7	119	13	DN773586
C 29	24.2	9.6	83	12	EC134983
C 30	24.2	9.6	104	9	CN071764
C 31	24.2	9.6	115	17	CW117487
C 32	24.2	9.6	117	18	DU188381
C 33	24	9.5	92	16	BZ585533
C 34	24	9.5	100	9	CK005996
C 35	24	9.5	100	17	CL952595
C 36	24	9.5	101	8	CD029354
C 37	24	9.5	102	16	CC376448
C 38	24	9.5	105	9	CK451897
C 39	24	9.5	116	8	CF741809
C 40	23.8	9.4	85	12	EC429664
C 41	23.8	9.4	93	9	CK100624
C 42	23.8	9.4	101	3	BJ965328
C 43	23.8	9.4	102	3	BJ965717
C 44	23.8	9.4	102	3	BJ970068
C 45	23.8	9.4	103	3	BJ967675

## ALIGNMENTS

RESULT 1  
AZ769498  
LOCUS  
DEFINITION 1M0570K16F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0570K16 F, genomic survey sequence.  
ACCESSION AZ769498  
VERSION AZ769498.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 100)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 100.  
Location/Qualifiers  
1. 100  
/organism="Mus musculus"

/mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0570K16"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 11.5%; Score 29; DB 15; Length 100;  
 Best Local Similarity 71.7%; Pred. No. 3.6e+03;  
 Matches 38; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
 Qy 147 GAGCCACAGACGTCGACAGTCCGGCAGCGAGCGGGGAGAGCAGCGGCT 199  
 Db 23 GCGCAGGTGAGCGCTCCGCCCGGGGAGAGCGGGGAGAGCGCGGCT 75

## RESULT 2

EC491510/c  
 LOCUS  
 DEFINITION EC491510 103 bp mRNA linear EST 22-JUN-2006  
 IT189508 0197\_3386 LNCAP + R1881 synthetic Androgen human prostate  
 library Homo sapiens cDNA similar to  
 ENSG00000197152|ENST00000356485, mRNA sequence.

## ACCESSION

VERSION EC491510.1 GI:109531102  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Bainbridge,M.N., Warren,R.L., Hirst,M., Romanuk,T., Zeng,T.,  
 Go.A., Delany,A., Griffith,M., Hickenbotham,M., Magrini,V,  
 Mardis,E.R., Sadar,M.D., Siddiqui,A.S., Marra,M.A. and Jones,S.J.M.

## TITLE

Analysis of the prostate cancer cell line LNCap transcriptome using  
 a sequencing-by-synthesis approach

## JOURNAL

COMMENT Unpublished (2006)

## CONTACT

Contact: Steven Jones  
 Bioinformatics  
 British Columbia Genome Sciences Centre  
 Email: sjones@bcgsc.ca  
 EST was generated using 454 life sciences sequence-by-synthesis  
 sequencer.

## FEATURES

## source

## Location/Qualifiers

1..103

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/sex="male"

/tissue\_type="prostate"

/cell\_line="LNCap"

/clone\_lib="LNCAP + R1881 synthetic Androgen human

## prostate library"

/note="LNCap human prostate cancer cells (American Type Culture Collection; Bethesda, MD) were maintained in RPMI-1640 media (StemCell Technologies; Vancouver, BC) supplemented with 10% fetal bovine serum (FBS; StemCell Technologies) and incubated at 37C with 5% CO2. Cells at passage 38 were plated at a density of approximately 4x10<sup>6</sup> cells per T175 flask. Cells were serum-starved for 48 hours prior to treatment for 16 hours with 10 nM R1881 (PerkinElmer; Woodbridge, Canada). Cells were harvested and total RNA was extracted from the cells using TRIzol Reagent (Invitrogen Life Technologies, Carlsbad, CA) following the manufacturer's instructions"

## ORIGIN

Query Match 11.3%; Score 28.6; DB 12; Length 103;  
 Best Local Similarity 57.1%; Pred. No. 4.7e+03;  
 Matches 52; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 39 CCAAGTTGGAAGGGCGTTTCTGTTTCTGATGACAGAGTCTCTGACTCTCTCG 98  
 Db 103 CCTGTTGGCAGACTGCTTTTTTTTTTTTGTAGACGGAGTCTTGTGCTCTCAG 44

Qy 99 CCACGGCTGAGTTCCGGCTCCAGGTTCCG 129

Db 43 GCTGGAGTCAGTGGCCTGATCTCGGCTCAC 13

## RESULT 3

## EC465112/c

## LOCUS

## DEFINITION

EC465112 97 bp mRNA linear EST 21-JUN-2006

2T010516 3708 0837 LNCAP + R1881 synthetic Androgen human prostate

library Homo sapiens cDNA similar to

ENSG00000077235|ENST00000356183, mRNA sequence.

## ACCESSION

VERSION EC465112.1 GI:109429135

## KEYWORDS

SOURCE EST.

## ORGANISM

Homo sapiens (human)

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Bainbridge,M.N., Warren,R.L., Hirst,M., Romanuk,T., Zeng,T.,

Go.A., Delany,A., Griffith,M., Hickenbotham,M., Magrini,V,

Mardis,E.R., Sadar,M.D., Siddiqui,A.S., Marra,M.A. and Jones,S.J.M.

Analysis of the prostate cancer cell line LNCap transcriptome using

a sequencing-by-synthesis approach

Unpublished (2006)

Contact: Steven Jones

Bioinformatics

British Columbia Genome Sciences Centre

Email: sjones@bcgsc.ca

EST was generated using 454 life sciences sequence-by-synthesis

sequencer.

## FEATURES

## source

## Location/Qualifiers

1..97

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/sex="male"

/tissue\_type="prostate"

/cell\_line="LNCap"

/clone\_lib="LNCAP + R1881 synthetic Androgen human

prostate library"

/note="LNCap human prostate cancer cells (American Type

Culture Collection; Bethesda, MD) were maintained in

RPMI-1640 media (StemCell Technologies; Vancouver, BC)

supplemented with 10% fetal bovine serum (FBS; StemCell

Technologies) and incubated at 37C with 5% CO2. Cells at

passage 38 were plated at a density of approximately

4x10<sup>6</sup> cells per T175 flask. Cells were serum-starved for

48 hours prior to treatment for 16 hours with 10 nM R1881

(PerkinElmer; Woodbridge, Canada). Cells were harvested and total RNA was extracted from the cells using TRIzol Reagent (Invitrogen Life Technologies, Carlsbad, CA) following the manufacturer's instructions"

ORIGIN  
Query Match 11.1%; Score 28; DB 12; Length 97;  
Best Local Similarity 58.3%; Pred. No. 6.9e+03;  
Matches 49; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
QY 128 GCGTGTGCGCCCTGAGGTTGAGGCGACAGACTCGCAGTCGGCAGGAGGCGGGGAG 187  
DB 88 GTGTGCTTGAGATCTTGGAGCATATACACGGTGTGGATGACAGAGGAGCTG 29  
QY 188 AGACGAGCGGCTTGGCCCTTAA 211  
DB 28 CGACAGACGGTTCTCGGACCTTAA 5

RESULT 4  
CG574657 103 bp mRNA linear GSS 02-OCT-2003  
LOCUS OST207730 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST207730,  
DEFINITION mRNA sequence.  
ACCESSION CG574657  
VERSION CG574657.1 GI:37364994  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 103)  
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
Piggott, J., BeltrandeRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Friddie, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
Key, B.W., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C. and Sands, A.T.

TITLE Wk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
PUBMED 14610273

COMMENT Contact: Zambrowicz BP  
OmniBank

Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com  
Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.

FEATURES  
source Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129Sv/Ev"  
/db\_xref="taxon:10090"  
/clone="OST207730"  
/cell\_type="embryonic stem cell"  
/clone\_lib="Mus musculus 129Sv/Ev"

ORIGIN  
Query Match 11.0%; Score 27.6; DB 17; Length 103;  
Best Local Similarity 67.2%; Pred. No. 8.9e+03;  
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 39 CCAAGTTGGAGGCGCTTGTCTTCTTTCTGATGCAGAGTCCTGACTCCCTC 96  
DB 42 CCAACTGTAGAGCACTGAGGTTCTTCTGATCAAGCGTCTTACTGCTTC 99

RESULT 5

EE366986

LOCUS LB02989.CR\_P21 GC\_BGC-29 Bos taurus cDNA clone IMAGE:8486471, mRNA  
DEFINITION sequence.  
ACCESSION EE366986  
VERSION EE366986.1 GI:112227366  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 110)

REFERENCE  
AUTHORS Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y.,  
Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C.,  
Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakaliff, R.,  
Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R.,  
Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R.R., Stott, J.,  
Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A.

TITLE Bovine Genome Sequencing Program: Full-length cDNA Sequencing  
JOURNAL Unpublished (2005)  
COMMENT Contact: Robert Kirkpatrick  
Canada's Michael Smith Genome Sciences Centre  
BC Cancer Agency  
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,  
Canada, V5Z 4S6  
Tel: 1-604-707-5900 x5406  
Fax: 1-604-876-3561  
Email: robertk@bcgc.ca  
Plate: LB02989 row: P column: 21  
High quality sequence stop: 110.  
Location/Qualifiers  
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/clone="IMAGE:8486471"  
/sex="male"  
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/dev\_stage="6 months old fetus"  
/lab\_host="E. coli DH10B T1 Phage resistant"  
/clone\_lib="GC BGC-29"  
/note="Vector: pExpress 1; Site 1: Blunt (5' end of cDNA);  
Site 2: NotI (3' end of cDNA)"

TITLE  
JOURNAL  
COMMENT

Contact: Robert Kirkpatrick

Canada's Michael Smith Genome Sciences Centre

BC Cancer Agency

Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,

Canada, V5Z 4S6

Tel: 1-604-707-5900 x5406

Fax: 1-604-876-3561

Email: robertk@bcgc.ca

Plate: LB02989 row: P column: 21

High quality sequence stop: 110.

Location/Qualifiers

source

1..110

/organism="Bos taurus"

/mol\_type="mRNA"

/strain="Li Hereford"

/db\_xref="taxon:9913"

/clone="IMAGE:8486471"

/sex="male"

/tissue\_type="Skin"

/dev\_stage="6 months old fetus"

/lab\_host="E. coli DH10B T1 Phage resistant"

/clone\_lib="GC BGC-29"

/note="Vector: pExpress 1; Site 1: Blunt (5' end of cDNA);

Site 2: NotI (3' end of cDNA)"

ORIGIN

Query Match 10.7%; Score 27; DB 11; Length 110;  
Best Local Similarity 54.5%; Pred. No. 1.3e+04;  
Matches 54; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 92 CCCTCTGCCAGCGGTGAGTTCCGGCTCCAGTTCGGTTCGCCCTGAGGTTTGAGGC 151

DB 9 CGCTGACCGTGGGGGAAGCCCGAGCCGCCAAGTCCCTTCGCCCTCTCTTGGACC 68

QY 152 CAGACAGCTCGCAGTCGGCGCAGGAGGCGGGGAGAGA 190

DB 69 CTGACTGGAGCCCGCGGCTGGGTGGGGGGGAGGGA 107

RESULT 6

CG535738

LOCUS OST122945 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST122945,  
DEFINITION mRNA sequence.

ACCESSION CG535738

VERSION CG535738.1 GI:37322310

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 110)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

REFERENCE
AUTHORS 1 (bases 1 to 82)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandeRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Spark,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
PUBMED 14610273
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
source Location/Qualifiers
1..82
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST122945"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
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Query Match 10.4%; Score 26.2; DB 17; Length 82;
Best Local Similarity 56.6%; Pred. No. 2.1e+04;
Matches 43; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
Qy 64 TGTTCGTGATGCAGAGTCCTCTGACTCCCTCTGACCGGCTGAGTTTCGGCTCCAG 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6 TGTTCGTGATGCAGAGTCCTCTGACTCCCTCTGACCGGCTGAGTTTCGGCTCCAG 65
Qy 124 GTTCGGGTGCGCCT 139
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
66 CTGATATGAGGCCCT 81
RESULT 7
EC566335/c
LOCUS 93 bp mRNA linear EST 22-JUN-2006
DEFINITION I7283656.0934 2562 LNCAP + R1881 synthetic Androgen human prostate
library Homo sapiens cDNA similar to
ENSG00000166548|ENST00000299697, mRNA sequence.
ACCESSION EC566335
VERSION EC566335.1 GI:109605929
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 93)
Bainbridge,M.N., Warren,R.L., Hirst,M., Romanuk,T., Zeng,T.,
Go,A., Delany,A., Griffith,M., Hickenbotham,M., Magrini,V.,
Mardis,E.R., Sadar,M.D., Siddiqui,A.S., Marra,M.A. and Jones,S.J.M.
TITLE Analysis of the prostate cancer cell line LNCap transcriptome using
a sequencing-by-synthesis approach
JOURNAL Unpublished (2006)
COMMENT Contact: Steven Jones
Bioinformatics
British Columbia Genome Sciences Centre
Email: sjones@bcgsc.ca
EST was generated using 454 life sciences sequence-by-synthesis
sequencer.
FEATURES
source Location/Qualifiers
1..93

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/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="male"
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/cell_line="LNCap"
/clone_lib="LNCAP + R1881 synthetic Androgen human
prostate library"
/notes="LNCAP human prostate cancer cells (American Type
Culture Collection; Bethesda, MD) were maintained in
RPMI-1640 media (StemCell Technologies; Vancouver, BC)
supplemented with 10% fetal bovine serum (FBS; StemCell
Technologies) and incubated at 37C with 5% CO2. Cells at
passage 38 were plated at a density of approximately
4x10^6 cells per T175 flask. Cells were serum-starved for
48 hours prior to treatment for 16 hours with 10 nM R1881
(perkinElmer; Woodbridge, Canada). Cells were harvested
and total RNA was extracted from the cells using TRIzol
Reagent (Invitrogen Life Technologies, Carlsbad, CA)
following the manufacturer's instructions"
ORIGIN
Query Match 10.2%; Score 25.8; DB 11; Length 93;
Best Local Similarity 58.4%; Pred. No. 2.8e+04;
Matches 45; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Qy 66 TTTTCGTGATGCAGAGTCCTCTGACTCCCTCTGACCGGCTGAGTTTCGGCTCCAGGT 125
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
85 TTGCCTGGCTGCTCTCTCTTCTGAGAGCTGTTCCACCGCCTCTCTCCGGTTGGAGGC 26
Qy 126 TCGGTGTGCGCCCTGAG 142
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
25 TCTCATGTCTCTTTGGG 9
RESULT 8
CK014560/c
LOCUS 110 bp mRNA linear EST 04-FEB-2005
DEFINITION 33148rsicf_6492.y1 Oryza sativa cv. PA64s panicle sterile cDNA
library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
sequence.
ACCESSION CK014560
VERSION CK014560.1 GI:58604032
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 110)
AUTHORS Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,
Lv,H., Li,J., Wang,J., Deng,J., Ran,L., Shi,X., Wang,X., Wu,Q.,
Li,C., Ren,X., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
Wu,S. and Liu,J.
TITLE The Genomes of Oryza sativa: A History of Duplications
JOURNAL PLoS Biol. 3 (2), e38 (2005)
PUBMED 15685292
COMMENT Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhoyuan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 110
POLYA=No.
FEATURES
source Location/Qualifiers
1..110
/organism="Oryza sativa (indica cultivar-group)"

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/mol type="mRNA"
/db_xref="taxon:39946"
/tissue type="panicle"
/cell type="sterile"
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/clone_lib="Oryza sativa cv. PA64s panicle sterile cDNA
library"

ORIGIN
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Best Local Similarity 60.9%; Pred. No. 2.8e+04;
Matches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 127 CGCGTGTGCGCCCTTGGAGTTTGAGCCACAGCTCGCAGTGGCGAGGGGGGGGA 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 CGCAGCGCGCCCTTTCAGCTTGAGGCGCCACATGCGCGCGGAGATGGGGAGGA 18

Qy 187 GAGAGGAGC 195
    ||| ||| |||
Db 17 GAGAGAAGC 9

RESULT 9
CL952591/c
LOCUS      CL952591.1 110 bp DNA linear GSS 21-SEP-2004
DEFINITION OsrIRUA01748 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
ACCESSION  CL952591
VERSION     CL952591.1 GI:52364600
SOURCE      Oryza sativa (indica cultivar-group)
ORGANISM    Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 110)
AUTHORS    Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE      An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL    Unpublished (2004)
COMMENT    Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
            Chinese Academy of Sciences, Beijing 101300, China
            Tel: 86-10-80481559
            Fax: 86-10-80488676
            Email: chenchen@genomics.org.cn
            Rice genomic sequence.
            Class: exon-trapped.

FEATURES
source      1..110
            /organism="Oryza sativa (indica cultivar-group)"
            /mol type="genomic DNA"
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            /clone_lib="Oryza sativa Express Library"
            /notes="Oryza sativa exon trapped genomic sequences"

ORIGIN
Query Match      10.2%; Score 25.8; DB 17; Length 110;
Best Local Similarity 60.9%; Pred. No. 2.8e+04;
Matches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 127 CGCGTGTGCGCCCTTGGAGTTTGAGCCACAGCTCGCAGTGGCGAGGGGGGGGA 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 CGCAGCGCGCCCTTTCAGCTTGAGGCGCCACATGCGCGCGGAGATGGGGAGGA 18

Qy 187 GAGAGGAGC 195
    ||| ||| |||
Db 17 GAGAGAAGC 9

RESULT 10
EB652145/c
LOCUS      EB652145.1 111 bp mRNA linear EST 25-APR-2006
DEFINITION GmUSCLMBHI03pTriplex214j07f1 Gillichthys mixed tissue (liver,
muscle, brain, heart, intestine) library 2 Gillichthys mirabilis
cDNA clone 14j07 5', mRNA sequence.
ACCESSION  EB652145
VERSION     EB652145.1 GI:93277671
SOURCE      Gillichthys mirabilis (long-jawed mudsucker)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Gobioidae; Gobiidae; Gillichthys.
REFERENCE   1 (bases 1 to 111)
AUTHORS    Gracey,A.Y.
TITLE      Unpublished, Andrew Y. Gracey
JOURNAL    Unpublished (2006)
COMMENT    Contact: Andrew Y. Gracey
            Biological Sciences
            University of Southern California
            3616 Trousdale Parkway #107, Mail Code 0371, Los Angeles, CA 90089,
            USA
            Tel: 213-740-2288
            Fax: 213-740-8123
            Email: Gracey@usc.edu
            Vector has been trimmed from this EST.
            Plate: 14 row: j column: 07
            Seq primer: Triplex 5' LD (5'-CTCGGAAGCGCCCATGTGTGGT-3')
            High quality sequence stop: 111.

FEATURES
source      1..111
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            /tissue type="Liver, muscle, brain, heart, intestine"
            /dev stage="Adult"
            /lab host="E.coli Electromax DH10B"
            /clone_lib="Gillichthys mixed tissue (liver, muscle,
            brain, heart, intestine) library 2"
            /notes="Vector: pTriplex2; Site 1: Sfil GGCCATTACGGCC;
            Site 2: Sfil GGCGCTTCGGCC; Normalized and serially
            subtraced cDNA library prepared from environmentally
            challenged animals"

ORIGIN
Query Match      10.2%; Score 25.8; DB 12; Length 111;
Best Local Similarity 56.5%; Pred. No. 2.8e+04;
Matches 48; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 137 CCTGAGTTTCAGGCGCAGACAGCTCGCAGTCGGCGGAGGAGGAGAGAGAGCG 196
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 107 CCTGCTTCTGATCCACATCTGCTGGAAGTGGCGAGAGCGCAGAGATGGATGATG 48

Qy 197 GCTCTGCGCCCTTAATTGTTACTTCG 221
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 AGTCTGCGCCATCCATCGTCGCGCG 23

RESULT 11
EC536793
LOCUS      EC536793 113 bp mRNA linear EST 22-JUN-2006
DEFINITION 17264505.0517 1775 LNCAP + R1881 synthetic Androgen human prostate
library Homo sapiens cDNA similar to
ENSG00000176095|ENST00000321599, mRNA sequence.
ACCESSION  EC536793
VERSION     EC536793.1 GI:109576387
KEYWORDS    EST.
SOURCE      Homo sapiens (human)

```

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 113)  
 AUTHORS Bainbridge, M.N., Warren, R.L., Hirst, M., Romanuk, T., Zeng, T.,  
 Go, A., Delany, A., Griffith, M., Hickenbotham, M., Magrini, V.,  
 Mardis, E.R., Sadar, M.D., Siddiqui, A.S., Marra, M.A., and Jones, S.J.M.  
 TITLE Analysis of the prostate cancer cell line LNCap transcriptome using  
 a sequencing-by-synthesis approach  
 JOURNAL Unpublished (2006)  
 COMMENT Contact: Steven Jones  
 Bioinformatics  
 British Columbia Genome Sciences Centre  
 Email: sjones@bcgsc.ca  
 EST was generated using 454 life sciences sequence-by-synthesis  
 sequencer.

Location/Qualifiers  
 1. 113  
 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /sex="male"  
 /tissue\_type="prostate"  
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 /clone\_lib="LNCap + R1881 synthetic Androgen human  
 prostate library"  
 /note="LNCap human prostate cancer cells (American Type  
 Culture Collection; Bethesda, MD) were maintained in  
 RPMI-1640 media (StemCell Technologies; Vancouver, BC)  
 supplemented with 10% fetal bovine serum (FBS; StemCell  
 Technologies) and incubated at 37C with 5% CO2. Cells at  
 passage 38 were plated at a density of approximately  
 4x10<sup>6</sup> cells per T175 flask. Cells were serum-starved for  
 48 hours prior to treatment for 16 hours with 10 nM R1881  
 (PerkinElmer; Woodbridge, Canada). Cells were harvested  
 and total RNA was extracted from the cells using TRIzol  
 Reagent (Invitrogen Life Technologies, Carlsbad, CA)  
 following the manufacturer's instructions"

## FEATURES

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1. 113  
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 /clone\_lib="LNCap + R1881 synthetic Androgen human  
 prostate library"  
 /note="LNCap human prostate cancer cells (American Type  
 Culture Collection; Bethesda, MD) were maintained in  
 RPMI-1640 media (StemCell Technologies; Vancouver, BC)  
 supplemented with 10% fetal bovine serum (FBS; StemCell  
 Technologies) and incubated at 37C with 5% CO2. Cells at  
 passage 38 were plated at a density of approximately  
 4x10<sup>6</sup> cells per T175 flask. Cells were serum-starved for  
 48 hours prior to treatment for 16 hours with 10 nM R1881  
 (PerkinElmer; Woodbridge, Canada). Cells were harvested  
 and total RNA was extracted from the cells using TRIzol  
 Reagent (Invitrogen Life Technologies, Carlsbad, CA)  
 following the manufacturer's instructions"

Query Match 10.2%; Score 25.8; DB 12; Length 113;  
 Best Local Similarity 58.4%; Pred. No. 2.8e+04;  
 Matches 45; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 7 TCTGCACTGAGAGGGCTGTTAAGGCTCCCAAGTTGGAAGGCGCTTGTCTCT 66  
 Db 17 TCTTTTGTCTTCGGGGAACTGTAAGCCCTCGCTTCTGGGAATCGCTCTGTGCTCT 76  
 Qy 67 TTTCTGGATGCAGATC 83  
 Db 77 TTCTGGAAGCTAGCC 93

## ORIGIN

Query Match 10.2%; Score 25.8; DB 12; Length 113;  
 Best Local Similarity 58.4%; Pred. No. 2.8e+04;  
 Matches 45; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 7 TCTGCACTGAGAGGGCTGTTAAGGCTCCCAAGTTGGAAGGCGCTTGTCTCT 66  
 Db 17 TCTTTTGTCTTCGGGGAACTGTAAGCCCTCGCTTCTGGGAATCGCTCTGTGCTCT 76  
 Qy 67 TTTCTGGATGCAGATC 83  
 Db 77 TTCTGGAAGCTAGCC 93

RESULT 12  
 AV841732  
 LOCUS AV841732 Nori Satoh unpublished cDNA library, egg Ciona  
 DEFINITION intestinalis cDNA clone rcieg05m22, mRNA sequence.

ACCESSION AV841732  
 VERSION AV841732.1 GI:16785883  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis  
 ORGANISM Ciona intestinalis

REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Clonidae; Ciona.  
 AUTHORS 1 (bases 1 to 99)  
 TITLE Expressed genes in Ciona intestinalis

UNPUBLISHED (2000)  
 COMMENT Contact: Nori Satoh  
 Department of Zoology  
 Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4081  
 Fax: 81-75-705-1113  
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

## FEATURES

## source

1. 99  
 /organism="Ciona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="rcieg05m22"  
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## ORIGIN

Query Match 10.2%; Score 25.6; DB 7; Length 99;  
 Best Local Similarity 66.1%; Pred. No. 3.2e+04;  
 Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 8 CTCGAACGTAGAGGGCTGTTAAGGCTCCCAAGTTGGAAGGCGCTTGTCTTC 63  
 Db 16 CTTGCTTAAGTGGGTTGAATGGGTTTCCCAATTTGAGGGTGACTTTGCTTC 71

## RESULT 13

## LOCUS

DU408432  
 DEFINITION 1098474026684 CHORI-243 Ovis aries genomic clone CH243-202P18,  
 genomic survey sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## Ovis aries

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Caprinae; Ovis.

## REFERENCE 1 (bases 1 to 103)

## AUTHORS

Kirkness, E., Shetty, J., de Jong, P., McEwan, J.C., Oddy, H. and  
 Cockett, N.

## TITLE

## Ovine BAC End Sequences from Library CHORI-243

## JOURNAL

## UNPUBLISHED (2004)

## COMMENT

## Other\_GSSs: 1098474028028

## Contact: Even Kirkness

## The Institute for Genomic Research (TIGR; www.tigr.org)

## 9712 Medical Center Drive, Rockville, MD 20850, USA

## Tel: 301-795-7536

## Email: ekirknes@tigr.org

## Sequences generated at the J. Craig Venter Institute Joint

## Technology Center (JCVITC; http://www.venterinstitute.org/).

## Original Trace: 1098474026684 Trace TT: gnl|ti|918952333

## Insert Length: 184000 Std Error: 0.00 row: P column: 18

## Seq primer: SP6

## Class: BAC ends.

## Location/Qualifiers

## 1. 103

## /organism="Ovis aries"

## /mol\_type="genomic DNA"

## /strains="Texel breed"

## /db\_xref="taxon:9940"

## /clone="CH243-202P18"

## /sex="Male"

## /cell\_type="Blood"

## /clone\_lib="CHORI-243"

/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;  
 The CHORI-243 sheep (M) (Ovis aries) BAC library produced  
 by Pieter de Jong's lab at CHORI  
 http://bacpac.chori.org/library.php?id=162"

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## 49; Conservative

## 0; Mismatches

## 39; Indels

## 0; Gaps

## 0;



Qy 64 TGTTCCTGATGAGAGTCTCTGACTCCCTCTGACCGGGCTGAGTTTCGGGCTCCAG 123  
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 Db 4 TGTGTTCAAAATGAGAAATCAGAAATGTCAATTTCCAGCTCTGCGGTGACGGGGCCGG 63  
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 Qy 124 GTTCGCGTGTGCGCCCTGAGGTTTGAGGC 151  
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 Db 64 GGTGGGGGGGAGGCTGGGGGTGAGGC 91  
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RESULT 14  
 CG255380/c  
 LOCUS CG255380 117 bp DNA linear GSS 25-AUG-2003  
 DEFINITION OGVCP92TH\_ZM\_0.7\_1.5\_KB\_Zea\_mays\_genomic\_clone\_ZMMBMA0505P16,  
 genomic survey sequence.

ACCESSION CG255380  
 VERSION CG255380.1 GI:34159750  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 117)  
 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
 Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.  
 TITLE Consortium for Maize Genomics  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Cathy Whitelaw

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TR  
 Class: methylation filtered.  
 Location/Qualifiers

FEATURES  
 source  
 1..117  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBMA0505P16"  
 /clone\_lib="ZM 0.7 1.5 KB"  
 /notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

ORIGIN  
 Query Match 10.2%; Score 25.6; DB 17; Length 117;  
 Best Local Similarity 57.5%; Pred. No. 3.2e+04;  
 Matches 46; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 128 GCGTGTGCGCCCTGAGTTTGAGCCAGACAGCTCGCAGTCGGCAGGAGGGGGGAG 187  
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 Db 104 GCGGTGCGGGCAGCGATGTGAAGCACGGCGGACATCTCGGTGCGGGGGCGGCCAG 45  
 |||||  
 Qy 188 AGACGAGCGGCTCTGGCCCC 207  
 |||||  
 Db 44 CGATGTGAAGCTCCGGCCTC 25  
 |||||

RESULT 15  
 AW800261/c  
 LOCUS AW800261 103 bp mRNA linear EST 16-MAY-2000  
 DEFINITION MR2-UM0060-170400-203-e06 UM0060 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AW800261  
 VERSION AW800261.1 GI:7852131  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;

Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS

1 (bases 1 to 103)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 PUBMED 10737800

COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil

Tel: +55-11-2704922  
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=et2=MR2-UM0060-170  
 400-203-e06&t3=2000-04-17&t4=1)

Seq primer: puc 18 forward  
 High quality sequence start: 9  
 High quality sequence stop: 80.

FEATURES  
 Location/Qualifiers

1..103  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="UM0060"  
 /note="Organ: uterus; Vector: puc18; Site 1: SmaI; Site 2:  
 SmaI; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No.  
 196,716 - Ludwig Institute for Cancer Research) profiles  
 into the pUC 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."

ORIGIN

Query Match 10.0%; Score 25.2; DB 7; Length 103;  
 Best Local Similarity 55.8%; Pred. No. 4.1e+04;  
 Matches 48; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 149 GGCACAGACGCTCGCAGTCGGGCGAGGAGGGGGGAGACGAGCGGCTTGGCCCT 208  
 |||||  
 Db 90 GGCACACAACTCGGAACTCGGTGGAGCTGAGGGTGAAGGGGAGTGCACAGACCATC 31  
 |||||  
 Qy 209 TAATTGTACTTCGGGCTCGTATTGTC 234  
 |||||  
 Db 30 CTTCTATAGCCAGGTAACTTTTGTG 5  
 |||||

Search completed: June 19, 2007, 17:02:10  
 Job time : 12312 secs

GenCore version 6.2.1  
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OM nucleic : nucleic search, using sw model

Run on: June 19, 2007, 13:59:45 ; Search time 2184 Seconds  
(without alignments)  
2500.230 Million cell updates/sec

Title: US-10-604-726A-5135  
Perfect score: 79  
Sequence: 1 ggaaggcggggagagacga.....ucucuccuucgcccaccucc 79

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 3761712

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_hg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.2	25.6	49	2	AX772410 Sequence
C 2	19.8	25.1	63	2	E08253 linker. 11/
C 3	19.2	24.3	51	2	AX898740 Sequence
C 4	19.2	24.3	51	2	BD034273 Sequence
C 5	19.2	24.3	51	2	AR734534 Sequence
6	19	24.1	65	2	E08252 linker. 11/
C 7	19	24.1	65	2	AX184576 Sequence
8	18.8	23.8	39	2	A86879 Sequence 19
9	18.8	23.8	39	2	BD070385 Factor X-
10	18.8	23.8	39	2	AR340859 Sequence
C 11	18.8	23.8	54	2	AR118827 Sequence
C 12	18.8	23.8	72	2	CS254876 Sequence
C 13	18.8	23.8	79	2	AR126073 Sequence
C 14	18.6	23.5	55	2	BD270121 Method of
C 15	18.6	23.5	65	2	BD464871 OLIGONUCL
C 16	18.6	23.5	65	2	CQ534358 Sequence
C 17	18.6	23.5	69	6	MMTRB138 Mouse mRNA
C 18	18.6	23.5	74	5	M18023 Human DNA t

19	18.4	23.3	62	2	AR166135 Sequence
20	18.4	23.3	62	2	AR235763 Sequence
21	18.4	23.3	62	2	AR236505 Sequence
22	18.4	23.3	62	2	AR279563 Sequence
23	18.4	23.3	65	2	AX899943 Sequence
24	18.4	23.3	65	2	BD035476 Sequence
25	18.4	23.3	65	2	AR735737 Sequence
26	18.4	23.3	80	2	BD411059 An Oligon
C 27	18.2	23.0	60	2	BD471330 OLIGONUCL
C 28	18.2	23.0	60	2	CQ540817 Sequence
29	18.2	23.0	65	2	A30344 Artificial
C 30	18.2	23.0	65	2	A30345 Artificial
31	18.2	23.0	65	2	BD461809 OLIGONUCL
32	18.2	23.0	65	2	CQ531296 Sequence
33	18.2	23.0	65	2	I11576 Sequence 28
C 34	18	22.8	40	2	BD298221 Apoptin r
C 35	18	22.8	40	2	AX092132 Sequence
C 36	18	22.8	40	2	AX138312 Sequence
C 37	18	22.8	42	2	AR241798 Sequence
C 38	18	22.8	50	2	CQ004542 Sequence
C 39	18	22.8	51	2	CQ002150 Sequence
C 40	18	22.8	51	2	CQ003187 Sequence
C 41	18	22.8	54	2	CQ861200 Sequence
C 42	18	22.8	78	2	AR031577 Sequence
C 43	18	22.8	78	2	AR065689 Sequence
C 44	18	22.8	78	2	AR097448 Sequence
C 45	18	22.8	78	2	I49966 Sequence 16

#### ALIGNMENTS

RESULT 1	AX772410	49 bp	DNA	linear	PAT 02-JUL-2003
AX772410	Sequence 200 from Patent WO03042407.				
LOCUS	AX772410				
DEFINITION	AX772410				
ACCESSION	AX772410.1	GI:32438983			
VERSION	AX772410.1	GI:32438983			
KEYWORDS	Drosophila melanogaster (fruit fly)				
SOURCE	Drosophila melanogaster				
ORGANISM	Drosophila melanogaster				
REFERENCE	Dickson B., Berger J., Suzuki T. and Knoblich J.				
AUTHORS	Method for identifying therapeutic targets by use of genetic				
TITLE	screens in drosophila melanogaster				
JOURNAL	Patent: WO 03042407-A 200 22-MAY-2003;				
BOEHRINGER INGELHEIM INTERNATIONAL GMBH; CD Patents (DE)					
FEATURES	Location/Qualifiers				
source	1..49				
	/organism="Drosophila melanogaster"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:7227"				
ORIGIN					
Query Match	25.6%	Score 20.2;	DB 2;	Length 49;	
Best Local Similarity	51.5%;	Pred. No. 2.5e+04;			
Matches	17;	Conservative	8;	Mismatches	8;
				Indels	0;
				Gaps	0;
QY	22	CGGCUCUGCCGCCUUAUUGACUUCGGGCGCG 54			
Db	6	CCCTTGTGCTCCCTCATTTAACTTCGGGTTCG 38			
RESULT 2	E08253	63 bp	DNA	linear	PAT 04-NOV-2005
E08253/c	linker.				
LOCUS	E08253				
DEFINITION	E08253				
ACCESSION	E08253.1	GI:2176374			
VERSION	E08253.1	GI:2176374			
KEYWORDS	JP 1994279497-A/12.				

44

Key	Location/Qualifiers
FT source	1. .39





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OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:52:37 ; Search time 314 Seconds  
(without alignments)  
1864.442 Million cell updates/sec

Title: US-10-604-726A-5135

Perfect score: 79

Sequence: 1 ggaaggcggggagagacga.....ucucuuuucgaccuuc 79

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 6021484

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_200701.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*
- 16: Geneseqn2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19.2	24.3	51	3 AAC10528	Aac10528 Human sec
C 2	19.2	24.3	80	12 ADM79864	Adm79864 DNA ligase
C 3	19.2	24.1	65	4 AAH68997	Aah68997 Human cer
C 4	18.8	23.8	39	2 AAV56769	Av56769 Human fac
C 5	18.8	23.8	72	6 AAD30987	Aad30987 Schizosac
C 6	18.8	23.8	72	6 AAD31044	Aad31044 Oligonuc
C 7	18.8	23.8	79	4 AAF70953	Aaf70953 bFGF DNA
C 8	18.8	23.8	80	2 AAT00367	Aat00367 Family 4
C 9	18.6	23.5	55	3 AAA09070	Aaa09070 Sense pri
C 10	18.6	23.5	65	6 ABN31245	Abn31245 Rat splc
C 11	18.6	23.5	70	15 AEG84737	Aeg84737 Hematolog
C 12	18.6	23.5	80	12 ADM95117	Adm95117 Rat anti
C 13	18.4	23.3	51	15 AEH27179	Aeh27179 Human acu
C 14	18.4	23.3	62	2 AAX59388	Aax59388 Saccharom
C 15	18.4	23.3	65	3 AAC11731	Aac11731 Human sec
C 16	18.4	23.3	80	12 ADP49484	Adp49484 Oligonuc
C 17	18.2	23.0	42	15 AEL27903	Ael27903 Primer fo

18	18.2	23.0	50	13	ADU25177	Adu25177 Retroelem
19	18.2	23.0	50	13	ADU22644	Adu22644 Human tra
C 20	18.2	23.0	60	6	ABN37704	Abn37704 Human spl
C 21	18.2	23.0	65	6	ABN28183	Abn28183 Rat prime
C 22	18	22.8	40	4	AAF55591	Aaf55591 PCR prime
C 23	18	22.8	40	5	AAF57180	Aaf57180 AAP-1 cDN
C 24	18	22.8	42	8	ABX79761	Abx79761 EST polym
C 25	18	22.8	50	4	AAI29974	Aai29974 Human SNP
C 26	18	22.8	51	4	AAI27582	Aai27582 Human SNP
C 27	18	22.8	51	4	AAI28619	Aai28619 Human SNP
C 28	18	22.8	54	13	ADR47436	Adr47436 Construct
C 29	18	22.8	80	12	ADM95450	Adm95450 Rat anti
C 30	17.8	22.5	44	15	AEJ90543	Aej90543 Strong co
C 31	17.8	22.5	44	15	AEJ90544	Aej90544 Respirato
C 32	17.8	22.5	57	15	AEJ95125	Aeg95125 Amyloid-b
C 33	17.8	22.5	60	14	ADY71737	Ady71737 Liver can
C 34	17.8	22.5	60	14	AEA35582	Aea35582 Analyte d
C 35	17.8	22.5	60	15	AEL53328	Ael53328 Murray re
C 36	17.8	22.5	60	15	AEL70698	Ael70698 Murray re
C 37	17.8	22.5	75	14	ACL60339	Act60339 Human col
C 38	17.6	22.3	50	6	ABZ00856	Abz00856 Human leu
C 39	17.6	22.3	59	2	AAV64733	Aav64733 HIV anti-
C 40	17.6	22.3	59	4	AAH24745	Aah24745 Nucleotid
C 41	17.6	22.3	59	8	ACA74051	Act74051 Hepatitis
C 42	17.6	22.3	59	14	AED30192	Aed30192 Antiviral
C 43	17.6	22.3	60	6	ABN59362	Abn59362 Human spl
C 44	17.6	22.3	60	6	ABN59239	Abn59239 Human spl
C 45	17.4	22.0	36	6	ABK15487	Abk15487 Urokinase

#### ALIGNMENTS

#### RESULT 1

AAC10528/C  
ID AAC10528 standard; cDNA; 51 BP.

XX AAC10528;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 14603.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
gene therapy; chromosome mapping; ss.

OS Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (CBST ) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 1; SEQ ID NO 14603; 71pp + Sequence Listing; English.

CC The present sequence is one of a large number of 5' ESTs derived from  
mRNAs encoding secreted proteins. No ORF has yet been conclusively  
identified within the present sequence. The 5' ESTs were prepared from  
total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
sequences usually correspond mainly to the 3' untranslated region (UTR)





Sequence 65 BP; 19 A; 17 C; 19 G; 4 T; 0 U; 6 Other;

**Best local similarity** 97.15% **Identical residues**

<b>Matches</b>	<b>15;</b>	<b>Conservative</b>	<b>10;</b>	<b>Mismatches</b>	<b>15;</b>	<b>Indels</b>	<b>0;</b>	<b>Gaps</b>	<b>0;</b>
----------------	------------	---------------------	------------	-------------------	------------	---------------	-----------	-------------	-----------

Db 44 TTTTCTTCGTCNTCGAANANTCTCTTCCTTCGCTNNCGCC 5

AAV56769  
ID AAV56769 standard; DNA; 39 BP.

AAV56769;

DT 27-NOV-1998 (first entry)

Human Factor X PCR primer #1017.

KW PCR primer; ss.

OS Synthetic.

Homo sapiens.

PN WQ9838317-A1.

PD 03-SEP-1998.

27-FEB-1998; 98WO-AT000045.

PR 27-FEB-1997; 97AT-00000335.

PA (IMMO) IMMUNO AG.

PI Himmelspach M, Schlokat U, Dorner F, Fisch A, Eibl J;

DR WPI; 1998-481211/41.

PT  
PT  
PT

Example 6; Page 41; 86pp; German.

region of the natural F10a activation cleavage site, a modification that creates a processing site for a protease that does not naturally cleave F10 in this region. The proteins are used to generate, *in vivo* or *in vitro*, F10a analogues that can be used to control bleeding and for treating defects of factors IX, VII or VIII, e.g. in haemophiliacs who have developed antibodies to factors VIII and/or IX. The encoding nucleic acid can be used in gene therapy of the same conditions. The analogues have high stability and can be activated without use of animal enzymes such as trypsin. Only activation is affected, their activity is the same as the natural factor. The analogues can be isolated as a pure single-chain pro-protein (not usually possible because of rapid processing of the native precursor) and this converted to two-chain form by subsequent

Db	72	CCTTAATGTTCTTCATCATAAATCCTTTTCTCTGTTGGGAATC	27
XX		bFGF DNA ligand #86.	
DE		Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular;	
XX		atherosclerosis; angioplasty; stability; ss.	
KW		Unidentified.	
XX		US6177557-B1.	
OS		23-JAN-2001.	
XX		05-AUG-1996; 96US-00687421.	
PN		11-JUN-1990; 90US-00536428.	
XX		10-JUN-1991; 91US-00714131.	
XX		06-NOV-1992; 92US-00973333.	
XX		10-FEB-1994; 94US-00195005.	
XX		28-MAR-1994; 94US-00219012.	
XX		(NEXS-) NEXSTAR PHARM INC.	
PA		Janjic N, Gold L, Tasset D;	
XX		WPI; 2001-158583/16.	
XX		Novel nucleic acid ligands to basic fibroblast growth factor that are	
XX		useful as inhibitors of basic fibroblast growth factors and 2'-amino	
PT		modified RNA ligands, exhibit increased in vivo stability.	
PT		Claim 1; Col 69-75; 153pp; English.	
XX		The present invention relates to a purified and isolated non-naturally	
XX		occurring DNA ligands to basic fibroblast growth factor (bFGF). The	
CC		ligands are useful as part of gene therapy treatments and for diagnosing	
CC		pathogenesis of vascular diseases including initiation and progression of	
CC		atherosclerosis, acute coronary syndromes, vein graft disease and	
CC		restenosis following coronary angioplasty. The ligands have improved	
CC		stability in vivo	
XX		Sequence 79 BP; 18 A; 25 C; 13 G; 23 T; 0 U; 0 Other;	
SQ		Query Match 23.8%; Score 18.8; DB 4; Length 79;	
		Best Local Similarity 38.7%; Pred. No. 1.1e+04;	
		Matches 24; Conservative 11; Mismatches 27; Indels 0; Gaps	
QY	17	ACGAGCGCUCGCGCCCUUAUUGUCGCGCUGAUUGUCUCCUUCGCCAC	66
Db	7	ACGATCTGACTAGGCACCTGCATAGGAGTACCGACTCGATGTATGTCTACCTAGCTTAC	66
QY	77	UC 78	
Db	67	TC 68	
DE		RESULT 8	
XX		AAT00367	
ID		AAT00367 standard; DNA; 80 BP.	
XX		AC AAT00367;	
XX		14-AUG-1996 (first entry)	
DT		Family 4 bFGF DNA ligand b10 (experiment 2).	
XX		Family 1; family 2; ligand; thrombin;	
KW		systematic evolution of ligands by exponential enrichment; SELEX;	
KW		heparin; selection; region of homology; inhibitor; ss.	
XX		Synthetic.	
XX		Key	
FT		misc feature 1..20	
FT		Location/Qualifiers	

FT /\*tag= a  
 FT /note= "Fixed region"  
 FT 21..58  
 FT /\*tag= b  
 FT /note= "Variable region"  
 FT 59..80  
 FT /\*tag= c  
 FT /note= "Fixed region"  
 FT 76  
 FT /\*tag= d  
 FT /note= "given in the specification as f"

XX WO9521853-A1.

XX 17-AUG-1995.

XX 06-FEB-1995; 95WO-US001458.

XX 10-FEB-1994; 94US-00195005.

XX 28-MAR-1994; 94US-00219012.

XX (NEXS-) NEXSTAR PHARM INC.

XX Janjic N, Gold L, Tasset D;

XX WPI; 1995-293073/38.

XX Identification of ligands to basic fibroblast growth factor and thrombin  
 XX - which can be modified for increased in vivo stability.

XX Claim 21; Page 108; 236pp; English.

XX The sequences given in AAT00282-394 represent DNA ligands to basic  
 CC fibroblast growth factor (bFGF). These sequences were isolated using the  
 CC primers and target regions given in AAQ98421-29 using systematic  
 CC evolution of ligands by exponential enrichment (SELEX). DNA templates  
 CC containing a region of 30 or 40 random nucleotides flanked by constant  
 CC sequence regions, were synthesized. The constant regions were designed to  
 CC be amplified by the primers. The primer 3p7.1PS has 2 biotin  
 CC phosphoramidites and two additional A residues covalently attached to its  
 CC 5' terminus during synthesis. The random region was generated by  
 CC utilising an equimolar mixture of the four nucleotides during oligo-  
 CC nucleotide synthesis. Three pools of ssDNA were created that contain  
 CC internal random regions. Each pool was incubated with bFGF at an excess  
 CC of DNA to target. DNA bound to bFGF were selected by filtration. The  
 CC selected single stranded DNA (ssDNA) was then amplified by PCR. A  
 CC significant improvement in affinity of DNA ligands was seen after 10  
 CC rounds of selection. Five distinct families of ssDNA were identified,  
 CC based on regions of homology. Some sequences showed no obvious homology  
 CC to the five families and are considered to be orphans

XX Sequence 80 BP; 18 A; 25 C; 13 G; 23 T; 0 U; 1 Other;

Query Match 23.8%; Score 18.8; DB 2; Length 80;

Best Local Similarity 38.7%; Pred. No. 1.1e+04;

Matches 24; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY 17 ACAGCGGCGUCGCCCCUUAUUGUACUUCGGGCGUUAUUGUCUCUCCUUCGCCACC 76

DB 7 ACAGTCTGATAGCCACCTGCATAGGAGTAGTCCGACTCCGATTGTATGCTACCTAGCTTAC 66

QY 77 UC 78

DB 67 TC 68

RESULT 9

AAA09070/c

ID AAA09070 standard; DNA; 55 BP.

XX AAA09070;

XX 10-AUG-2000 (first entry)

XX

DE Sense primer for PROEX-1-beta-synuclein delta 1 construction.

XX

KW NACP/alpha-synuclein; beta-synuclein; beta-synuclein delta 1; mutant;

KW

KW primer; neurodegenerative; Alzheimers disease; Parkinsons disease;

XX

OS Lewy body disease; ss.

OS

OS Homo sapiens.

XX

OS Synthetic.

XX

PN WO200020020-A2.

XX

PD 13-APR-2000.

XX

XX 06-OCT-1999; 99WO-US023134.

XX

XX 06-OCT-1998; 98US-0103310P.

XX

XX (REGC ) UNIV CALIFORNIA.

XX

XX Masliah E;

XX

XX WPI; 2000-303637/26.

XX

XX Screening treatments for neurodegenerative disease, such as Alzheimer's

XX

XX disease, comprises stimulating oxidative stress and measuring and

XX

XX aggregation of non-amyloid beta component /alpha-synuclein in neuronal

XX

XX cells.

XX

XX Disclosure; Page 45; 47pp; English.

XX

XX Human NACP/alpha-synuclein, human beta-synuclein and its mutants, beta-  
 CC synuclein delta 1 and 2 were produced using the PROEX-1 6xHis expression  
 CC system. PROEX-1-beta-synuclein delta 1 was constructed by a two step PCR  
 CC protocol. This sense primer, corresponding to amino acids 73-83 of alpha-  
 CC synuclein and amino acids 73-79 of beta-synuclein, was used with  
 CC antisense primer BSYNNOT (AAA09071) encoding amino acids 129-134 of beta-  
 CC synuclein and NotI site at its 5' end. The PCR product was combined to  
 CC the product generated by primers AAA09068-69 by using BSYNNDE (AAA09068)  
 CC and BSYNNOT. The invention concerns methods for screening treatments for,  
 CC and treatment of, neurodegenerative disease. The methods comprise  
 CC measuring aggregation of neurons of NACP/alpha-synuclein and stimulating  
 CC expression of a non-amyloidogenic protein in order to reduce the level of  
 CC aggregation. In the screening method, oxidative stress is stimulated in  
 CC the neuronal cells by introduction of metal ions and hydrogen peroxide.  
 CC The methods are useful for treating and screening treatments for  
 CC neurodegenerative disease consisting of Alzheimer's disease, Parkinson's  
 CC disease and Lewy body disease

XX Sequence 55 BP; 16 A; 11 C; 23 G; 5 T; 0 U; 0 Other;

Query Match 23.5%; Score 18.6; DB 3; Length 55;

Best Local Similarity 42.9%; Pred. No. 1.2e+04;

Matches 21; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 18 CGAGCGGCGUCGCCCCUUAUUGUACUUCGGGCGUUAUUGUCUCUCC 66

DB 49 CGATGTTCCCTGCCCCCTCCACTGCTCTCTGGCTACTGCTGTACACC 1

RESULT 10

ID ABN31245/c

ABN31245 standard; DNA; 65 BP.

XX ABN31245;

XX 15-JUL-2002 (first entry)

XX

XX Rat spliced transcript detection oligonucleotide SEQ ID NO:3993.

XX

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

XX

XX splice variant; transcriptome; oligonucleotide library; ss.

XX

OS Rattus norvegicus.  
 XX WO200210449-A2.  
 XX PD 07-FEB-2002.  
 XX PF 20-JUL-2001; 2001WO-IB001903.  
 XX PR 28-JUL-2000; 2000US-0221607P.  
 XX PR 02-MAY-2001; 2001US-0287724P.  
 XX PA (COMP-) COMPUGEN INC.  
 XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX WPI; 2002-257383/30.  
 XX PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 PS Example 1; SEQ ID NO 3993; 47pp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridising selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 65 BP; 13 A; 21 C; 19 G; 12 T; 0 U; 0 Other;  
 Query Match 23.5%; Score 18.6; DB 6; Length 65;  
 Best Local Similarity 63.6%; Pred. No. 1.2e+04;  
 Matches 21; Conservative 3; Mismatches 9; Indels 0; Gaps 0;  
 QY 3 AGGCGGGGAGAGACGAGCGGCGCUCUGGCCCCU 35  
 DB 40 AGCCTGAGGAGCAGAGGAGTGCGTCTGCGCCAT 8  
 RESULT 11  
 AEG84737  
 ID AEG84737 standard; DNA; 70 BP.  
 XX  
 AC AEG84737;  
 XX  
 DT 01-JUN-2006 (first entry)  
 XX  
 DE Hematological cancer profiling, HCP, 70mer probe SEQ ID NO 4293.  
 XX  
 KW cancer; cytostatic; neoplasm; lymphoma; leukemia; diagnosis;  
 KW ss; probe.  
 XX  
 OS Homo sapiens.

XX WO20006034573-A1.  
 XX PD 06-APR-2006.  
 XX PF 27-SEP-2005; 2005WO-CA001464.  
 XX PR 27-SEP-2004; 2004US-0613980P.  
 XX PA (MEDB-) MED BIOGENE INC.  
 XX PI Yoganathan T;  
 XX WPI; 2006-293215/30.  
 XX PT System for profiling hematological cancer, comprises probes complementary  
 PT to mRNA transcribed from candidate genes whose expression pattern is  
 PT indicative of a feature of the cancer e.g. MYH11.  
 XX  
 PS Claim 5; SEQ ID NO 4293; 356pp; English.  
 XX  
 CC The invention relates to a system for profiling hematological cancer,  
 CC comprises polynucleotide probes comprising a sequence corresponding to,  
 CC or complementary to, an mRNA transcribed from candidate genes whose  
 CC expression pattern is indicative of one or more feature of a  
 CC hematological cancer chosen from lymphoma and leukemia, e.g. MYH11 and  
 CC APC. The system is useful for profiling a hematological cancer chosen  
 CC from lymphoma and leukemia. The hematological cancer is a lymphoma chosen  
 CC from B-cell CLL/SLL, B-cell prolymphocytic leukemia, lymphoplasmacytic  
 CC lymphoma, splenic marginal zone B-cell lymphoma, nodal marginal zone B-  
 CC cell lymphoma, hairy cell leukemia, plasma cell myeloma/plasmacytoma, FL,  
 CC MCL, Burkitt's lymphoma, DLBCL, Hodgkin's lymphoma, lymphoblastic  
 CC lymphoma, ALCL, cutaneous T-cell lymphoma, mycosis fungoides/Sezary's  
 CC syndrome, peripheral T-cell lymphomas, angioimmunoblastic lymphoma,  
 CC angiocentric lymphoma (nasal T-cell lymphoma), intestinal T-cell  
 CC lymphoma, and adult T-cell lymphoma/leukemia. The hematological cancer is  
 CC a leukemia chosen from acute myelogenous leukemia, acute lymphocytic  
 CC leukemia, chronic myelogenous leukemia, and chronic lymphocytic leukemia.  
 CC The system is useful for the preparation of a nucleic acid array. The  
 CC system enables accurate diagnosis and risk assessment of the  
 CC hematological cancer. The present sequence represents a hematological  
 CC cancer profiling, HCP, 70mer probe.  
 XX  
 SQ Sequence 70 BP; 14 A; 21 C; 17 G; 18 T; 0 U; 0 Other;  
 Query Match 23.5%; Score 18.6; DB 15; Length 70;  
 Best Local Similarity 40.4%; Pred. No. 1.3e+04;  
 Matches 23; Conservative 10; Mismatches 24; Indels 0; Gaps 0;  
 QY 14 GAGACGAGCGGCGCUCUGGCCCCUUAUUGUACUUGCGGCGUGUAUUGUCUCUUC 70  
 DB 1 GAAAGGAGCAACACACTGCGCCCTAGGCGTGGCGTGGCCAGTTCTCTCTGCTC 57  
 RESULT 12  
 ADM95117/c  
 ID ADM95117 standard; DNA; 80 BP.  
 XX  
 AC ADM95117;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Rat antisense oligonucleotide #10.  
 XX  
 KW Rat; antisense oligonucleotide; ss; antisense RNA production; oncogenes;  
 KW tumour suppressor; cell cycle regulator; ion channel protein;  
 KW transport protein; intracellular signal transduction;  
 KW transcription factor; DNA-binding protein;  
 KW cell-cell communication protein; stress response gene;  
 KW apoptosis related gene; growth factor; chemokine; interleukin;  
 KW interferon; hormone; neurotransmitter; cell surface antigen;  
 KW cell adhesion molecule.  
 XX





GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 14:28:35 ; Search time 129 Seconds  
(without alignments)  
1145.873 Million cell updates/sec

Title: US-10-604-726A-5135

Perfect score: 79

Sequence: 1 ggaaggcgaggagagacga.....ucuccuucgaccucc 79

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1528742

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_NA.\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1/ COMB.seq.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5/ COMB.seq.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A/ COMB.seq.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B/ COMB.seq.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7/ COMB.seq.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H/ COMB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS/ COMB.seq.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP/ COMB.seq.\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE/ COMB.seq.\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	19.8	25.1	63	2	US-08-014-723-12	Sequence 12, Appl
C 2	19.8	25.1	63	2	US-08-110-011A-12	Sequence 12, Appl
C 3	19.2	24.3	51	3	US-09-513-999C-14603	Sequence 14603, A
C 4	19	24.1	65	2	US-08-014-723-11	Sequence 11, Appl
C 5	19	24.1	65	2	US-08-110-011A-11	Sequence 11, Appl
C 6	18.8	23.8	39	3	US-09-367-791A-19	Sequence 19, Appl
C 7	18.8	23.8	54	3	US-08-444-818-753	Sequence 753, App
C 8	18.8	23.8	79	3	US-08-687-421-415	Sequence 415, App
C 9	18.4	23.3	62	3	US-08-965-762-27	Sequence 27, Appl
C 10	18.4	23.3	62	3	US-09-911-927-27	Sequence 27, Appl
C 11	18.4	23.3	62	3	US-09-911-882-27	Sequence 27, Appl
C 12	18.4	23.3	62	3	US-09-911-888-27	Sequence 27, Appl
C 13	18.4	23.3	65	3	US-09-513-999C-15806	Sequence 15806, A
C 14	18.2	23.0	65	2	US-08-086-410-28	Sequence 28, Appl
C 15	18	22.8	42	3	US-09-475-947A-86	Sequence 86, Appl
C 16	18	22.8	78	2	US-08-090-193-16	Sequence 16, Appl
C 17	18	22.8	78	2	US-08-488-031-16	Sequence 16, Appl
C 18	18	22.8	78	2	US-08-486-569-16	Sequence 16, Appl
C 19	18	22.8	78	2	US-08-488-027-16	Sequence 16, Appl
C 20	18	22.8	78	2	US-08-090-192-16	Sequence 16, Appl
C 21	18	22.8	78	2	US-08-482-663-16	Sequence 16, Appl
C 22	18	22.8	78	3	US-08-482-658-16	Sequence 16, Appl
C 23	18	22.8	78	3	US-08-470-349-16	Sequence 16, Appl

C 24	18	22.8	78	3	US-08-475-610-16	Sequence 16, Appl
C 25	18	22.8	78	7	PCT-US92-00277-16	Sequence 16, Appl
C 26	18	22.8	78	7	PCT-US92-00277-16	Sequence 16, Appl
C 27	17.8	22.5	77	5	US-09-844-508-25	Sequence 25, Appl
C 28	17.6	22.3	50	3	US-10-131-827-847	Sequence 847, App
C 29	17.6	22.3	50	5	US-10-131-831-847	Sequence 847, App
C 30	17.6	22.3	59	2	US-08-790-963-53	Sequence 53, Appl
C 31	17.6	22.3	59	3	US-09-371-774-53	Sequence 53, Appl
C 32	17.6	22.3	59	3	US-09-875-082-53	Sequence 53, Appl
C 33	17.4	22.0	72	2	US-08-433-126A-13	Sequence 13, Appl
C 34	17.4	22.0	72	2	US-08-433-124A-13	Sequence 13, Appl
C 35	17.4	22.0	72	3	US-08-376-413A-13	Sequence 13, Appl
C 36	17.4	22.0	72	7	PCT-US96-06059-13	Sequence 13, Appl
C 37	17.2	21.8	54	3	US-09-621-976-13448	Sequence 13448, A
C 38	17.2	21.8	60	4	US-09-804-980-240	Sequence 240, App
C 39	17.2	21.8	65	3	US-09-564-805-7	Sequence 7, Appli
C 40	17.2	21.8	65	3	US-09-434-382-7	Sequence 7, Appli
C 41	17.2	21.8	72	3	US-09-275-850-137	Sequence 137, App
C 42	17.2	21.8	72	3	US-09-907-111-137	Sequence 137, App
C 43	17.2	21.8	78	3	US-09-513-999C-15701	Sequence 15701, A
C 44	17	21.5	43	3	US-09-281-481A-12	Sequence 12, Appl
C 45	17	21.5	43	3	US-09-281-481A-14	Sequence 14, Appl

#### ALIGNMENTS

RESULT 1  
US-08-014-723-12/c  
; Sequence 12, Application US/08014723  
; Patent No. 5273962  
; GENERAL INFORMATION:  
; APPLICANT: Doi, Takeshi  
; APPLICANT: Iwasaki, Akio  
; APPLICANT: Saino, Yushi  
; APPLICANT: Kimura, Shigeru  
; APPLICANT: Okuchi, Masao  
; TITLE OF INVENTION: Thrombin-Binding Substance and Process  
; TITLE OF INVENTION: For Preparing the Same  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
; CITY: Arlington  
; STATE: Virginia  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/014,723  
; FILING DATE: 19930208  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5273962man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 80-071-0 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)413-3000  
; TELEFAX: (703)413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 63 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-014-723-12





QY 3 AGGCGGGGAGACGAGCGGCGUCUGGCCCUUA 37  
 Db 30 AGGTCGACGACGAGCGGCGGCTGTGGCGACTGA 64

## RESULT 5

US-08-110-011A-11  
 ; Sequence 11, Application US/08110011A  
 ; Patent No. 5354664  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Doi, Takeshi  
 ; APPLICANT: Iwasaki, Akio  
 ; APPLICANT: Saino, Yushi  
 ; APPLICANT: Kimura, Shigeru  
 ; APPLICANT: Onkuchi, Masao  
 ; TITLE OF INVENTION: Thrombin-Binding Substance and Process  
 ; TITLE OF INVENTION: For Preparing the Same  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBION, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESSEE: P.C.  
 ; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; ZIP: 22202

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/110,011A  
 ; FILING DATE: 23-AUG-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 ; NAME: OBION, No. 5354664man P.

REGISTRATION NUMBER: 24,618  
 ; REFERENCE/DOCKET NUMBER: 80-073-0 DIV

TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703)413-3000

TELEFAX: (703)413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 65 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid;

DESCRIPTION: DNA (synthetic)

US-08-110-011A-11

Query Match 24.1%; Score 19; DB 2; Length 65;  
 Best Local Similarity 62.9%; Pred. No. 1.1e+03;  
 Matches 22; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 3 AGGCGGGGAGACGAGCGGCGUCUGGCCCUUA 37  
 Db 30 AGGTCGACGACGAGCGGCGGCTGTGGCGACTGA 64

## RESULT 6

US-09-367-791A-19  
 ; Sequence 19, Application US/09367791A  
 ; Patent No. 6573071

GENERAL INFORMATION:

APPLICANT: Himmelspach, Michele

Schlokat, Uwe

Dorner, Friedrich

Fisch, Andreas

Eibl, Johann

TITLE OF INVENTION: Factor X Analogues With

NUMBER OF SEQUENCES: 122  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

FILING DATE: 12-No. 6573071-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AT A 335/97

FILING DATE: 27-FEB-1997

APPLICATION NUMBER: WO PCT/AT98/00045

FILING DATE: 27-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Ausenhus, Scott L.

REGISTRATION NUMBER: 42,471

REFERENCE/DOCKET NUMBER: 20695D-000700US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-367-791A-19

Query Match 23.8%; Score 18.8; DB 3; Length 39;  
 Best Local Similarity 44.7%; Pred. No. 1.2e+03;  
 Matches 17; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 33 CCUUAUUGUACUUCGGGCGUUAUUGUCUCUCCUUC 70

Db 2 CCAGATCGATTCTCGTCTGCTGTCGCCCTCTC 39

## RESULT 7

US-08-444-818-753/c

; Sequence 753, Application US/08444818

; Patent No. 6150087

; GENERAL INFORMATION:

APPLICANT: Chien, David Y.

APPLICANT: Rutter, William J.

TITLE OF INVENTION: NANV Diagnostics and Vaccines

NUMBER OF SEQUENCES: 777

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: CA

COUNTRY: USA

ZIP: 94608-2916

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,818

```

1  FILING DATE:
2  CLASSIFICATION: 424
3  PRIOR APPLICATION DATA:
4  APPLICATION NUMBER: US/08/403,590
5  FILING DATE: 14-MAR-1995
6  ATTORNEY/AGENT INFORMATION:
7  NAME: Harbin, Alisa A.
8  REGISTRATION NUMBER: 33,895
9  REFERENCE/DOCKET NUMBER: 0110.002
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (508)359-3876
12 TELEFAX: (508)359-3885
13 INFORMATION FOR SEQ ID NO: 753:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 54 base pairs
16 TYPE: nucleic acid
17 STRANDEDNESS: single
18 TOPOLOGY: linear
19 MOLECULE TYPE: other nucleic acid
20 DESCRIPTION: /desc = "primer JHC 13"
21 US-08-444-818-753

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Query Match 23.8%; Score 18.8; DB 3; Length 54;  
Best Local Similarity 48.1%; Pred. No. 1.3e+03;  
Matches 26; Conservative 6; Mismatches 22; Indels 0; Gaps. 0;

RESULT 8  
US-08-687-421-415  
; Sequence 415, Application US/08687421  
; Patent No. 6177557  
; GENERAL INFORMATION:  
; APPLICANT: Gold, Larry  
; APPLICANT: Janjic, Nebojsa  
; APPLICANT: Tasset, Diane  
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND  
; TITLE OF INVENTION: THROMBIN  
; NUMBER OF SEQUENCES: 445  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/687,421  
; FILING DATE: 08-MAY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/195,005  
; FILING DATE: 10-FEBRUARY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: 22-APRIL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/219,012  
; FILING DATE: 28-MARCH-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/973,333  
; FILING DATE: 11-NOVEMBER-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/714,131

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; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX07/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 415:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-687-421-415

Query Match      23.8%; Score 18.8; DB 3; Length 79;
Best Local Similarity 38.7%; Pred. No. 1.4e+03;
Matches 24; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY      17   ACGAGGGGCUUCGGCCCUUAAUGUAUUUGGCGGUCGUUAUGUCUUCUUCGCCACC 76
          ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      7   ACGATCTGACTACCCACCTGCATAGGAGTACCGACTCCGATTGTATGTCACTTAGCTTAC 66

QY      77 UC 78
          :|
          67 TC 68

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RESULT 9
US-08-965-762-27
; Sequence 27, Application US/08965762
; Patent No. 6280963
; GENERAL INFORMATION:
; APPLICANT: Koltin, Yigal
; APPLICANT: Gavrias, Victoria
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
; FILE REFERENCE: 07334/062001
; CURRENT APPLICATION NUMBER: US/08/965,762
; CURRENT FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-08-965-762-27

```

Query Match	23.3%	Score 18.4	DB 3	Length 62;
Best Local Similarity	38.5%;	Pred. No. 1.9e+03;		
Matches 20;	Conservative	11;	Mismatches 21;	Indels 0;
Gaps	0			

  

Qy	27	CUGGCCCCUUAUUGUAUCUUGGGCCUGUAUGUCUCUCCUUUGCCACACUUC	78
Dh	8	CCGGCCGCATCATCAAGATCTCATGGTATTGACATTTCTCTTGCCCTCCFC	59

```

RESULT 10
US-09-911-927-27
; Sequence 27, Application US/09911927
; Patent No. 6461826
;
; GENERAL INFORMATION:
; APPLICANT: Koltin, Yigal
; APPLICANT: Gavrilas, Victoria
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
; FILE REFERENCE: 06286-062003
; CURRENT APPLICATION NUMBER: US/09/911.927
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 08/965,762
; PRIOR FILING DATE: 1997-11-07
;

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; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 62  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer for PCR  
US-09-911-927-27

Query Match 23.3%; Score 18.4; DB 3; Length 62;  
Best Local Similarity 38.5%; Pred. No. 1.9e+03;  
Matches 20; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 27 CUGGCCCUAAUUGUACUUGCGGCGUUAUUGUCUUCUUCGCGCACCU 78  
||| :  
Db 8 CCGGCCCATCATGCAAGATCCTGATGTTGATTCATTCCTTGGCCTCTC 59

## RESULT 11

US-09-911-882-27  
; Sequence 27, Application US/09911882  
; Patent No. 6465198  
; GENERAL INFORMATION:  
; APPLICANT: Koltin, Yigal  
; APPLICANT: Gavrias, Victoria  
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE  
; FILE REFERENCE: 06286-062004  
; CURRENT APPLICATION NUMBER: US/09/911.882  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 08/965,762  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 62  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer for PCR  
US-09-911-882-27

Query Match 23.3%; Score 18.4; DB 3; Length 62;  
Best Local Similarity 38.5%; Pred. No. 1.9e+03;  
Matches 20; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 27 CUGGCCCUAAUUGUACUUGCGGCGUUAUUGUCUUCUUCGCGCACCU 78  
||| :  
Db 8 CCGGCCCATCATGCAAGATCCTGATGTTGATTCATTCCTTGGCCTCTC 59

## RESULT 12

US-09-911-888-27  
; Sequence 27, Application US/09911888  
; Patent No. 6514715  
; GENERAL INFORMATION:  
; APPLICANT: Koltin, Yigal  
; APPLICANT: Gavrias, Victoria  
; TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE  
; FILE REFERENCE: 06286-062002  
; CURRENT APPLICATION NUMBER: US/09/911.888  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: US 08/965,762  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 62  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer for PCR  
US-09-911-888-27

Query Match 23.3%; Score 18.4; DB 3; Length 62;  
Best Local Similarity 38.5%; Pred. No. 1.9e+03;  
Matches 20; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 27 CUGGCCCUAAUUGUACUUGCGGCGUUAUUGUCUUCUUCGCGCACCU 78  
||| :  
Db 8 CCGGCCCATCATGCAAGATCCTGATGTTGATTCATTCCTTGGCCTCTC 59

## RESULT 13

US-09-513-999C-15806  
; Sequence 15806, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513.999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 15806  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-513-999C-15806

Query Match 23.3%; Score 18.4; DB 3; Length 65;  
Best Local Similarity 71.4%; Pred. No. 1.9e+03;  
Matches 20; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 6 GCGGGGAGACGAGCGGCGUCUGGCC 33  
||||| :  
Db 17 GCGGGGTGGAGACGCGGCTCTGTAC 44

## RESULT 14

US-08-086-410-28  
; Sequence 28, Application US/08086410  
; Patent No. 5407822  
; GENERAL INFORMATION:  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: LOISON, Gerard  
; APPLICANT: PESSEGUE, Bernard  
; APPLICANT: SHIRE, David  
; TITLE OF INVENTION: Artificial promoter for the expression  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: King Street Station, Suite 500, 1800 Diagonal  
; STREET: Road, PO Box 299  
; CITY: ALEXANDRIA  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/086.410  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,083

Search completed: June 19, 2007, 15:45:42  
Job time : 131 secs

; CURRENT APPLICATION NUMBER: US/10/448,250

CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/407,123  
FILING DATE: 04-Apr-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/367,791A  
FILING DATE: 12-No. US20030181381A1-1999  
APPLICATION NUMBER: AT A 335/97  
FILING DATE: 27-FEB-1997  
APPLICATION NUMBER: WO PCT/AT98/00045  
FILING DATE: 27-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,471  
REFERENCE/DOCKET NUMBER: 20695D-00070005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-407-123-19

Query Match 23.8%; Score 18.8; DB 7; Length 39;  
Best Local Similarity 44.7%; Pred. No. 7.6e+03;  
Matches 17; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 33 CCUUAUUGUACUUCGGGCGUAGUUGUCUCCUUCUUC 70  
DB 2 CCAGAATCGATTCTCGTGTGTGTGTGTGTGTGTGTGTCTC 39

RESULT 5  
US-09-918-740-15/c  
Sequence 15, Application US/09918740  
Publication No. US20030033626A1  
GENERAL INFORMATION:  
APPLICANT: Hahn, Frederick  
APPLICANT: Kuehnle, Adelheid  
TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways  
FILE REFERENCE: KAS-103XC1  
CURRENT APPLICATION NUMBER: US/09/918,740  
CURRENT FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: 60/221,703  
PRIOR FILING DATE: 2000-07-31  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 15  
LENGTH: 72  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide containing S. cerevisiae DNA  
US-09-918-740-15

Query Match 23.8%; Score 18.8; DB 3; Length 72;  
Best Local Similarity 28.3%; Pred. No. 8.2e+03;

CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/407,123  
FILING DATE: 04-Apr-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/367,791A  
FILING DATE: 12-No. US20030181381A1-1999  
APPLICATION NUMBER: AT A 335/97  
FILING DATE: 27-FEB-1997  
APPLICATION NUMBER: WO PCT/AT98/00045  
FILING DATE: 27-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,471  
REFERENCE/DOCKET NUMBER: 20695D-00070005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-407-123-19

Query Match 23.8%; Score 18.8; DB 7; Length 39;  
Best Local Similarity 44.7%; Pred. No. 7.6e+03;  
Matches 17; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 33 CCUUAUUGUACUUCGGGCGUAGUUGUCUCCUUCUUC 70  
DB 2 CCAGAATCGATTCTCGTGTGTGTGTGTGTGTGTGTGTCTC 39

RESULT 5  
US-09-918-740-15/c  
Sequence 15, Application US/09918740  
Publication No. US20030033626A1  
GENERAL INFORMATION:  
APPLICANT: Hahn, Frederick  
APPLICANT: Kuehnle, Adelheid  
TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways  
FILE REFERENCE: KAS-103XC1  
CURRENT APPLICATION NUMBER: US/09/918,740  
CURRENT FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: 60/221,703  
PRIOR FILING DATE: 2000-07-31  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 15  
LENGTH: 72  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide containing S. cerevisiae DNA  
US-09-918-740-15

Query Match 23.8%; Score 18.8; DB 3; Length 72;  
Best Local Similarity 28.3%; Pred. No. 8.2e+03;







Query Match 23.0%; Score 18.2; DB 16; Length 50;  
Best Local Similarity 35.9%; Pred. No. 1.3e+04;  
Matches 14; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

**QY** 41 GUACUUGGGGCGUAUUGUCUCUCUUUGGCCACUCC 79  
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**Dδ** 39 GTCTTCTTCTCTGTATCGTTTCATCTCTTTCCCACCTAC 1

**RESULT 15**

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US-09-908-975-10452/c
; Sequence 10452, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10452
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-10452

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Query Match      23.0%; Score 18.2; DB 3; Length 60;
Best Local Similarity 45.2%; Pred. No. 1.3e+04;
Matches 14; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
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**Qy**                    33 CCUAAUUGUACUUCGGGCTCGUAUUGUCUC 63  
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**Dd**                    53 CCTAGTTGTACATGTTGCACGAATGGCTC 23

Search completed: June 19, 2007, 15:35:39  
Job time : 745 secs

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 15:23:21 ; Search time 2967 Seconds  
(without alignments)  
274.926 Million cell updates/sec

Title: US-10-604-726A-5135  
Perfect score: 79  
Sequence: 1 99agggcg9gggagacga.....ucucuccuucgacaccucc 79

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Gapop 10.0 , Gapext 1.0

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Maximum Match 100%  
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Database : Published Applications NA New.\*

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- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
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- 17: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 18: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 19: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 20: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 22: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	32	40.5	32	11	US-10-536-560-26233
C 2	24.2	30.6	63	19	US-11-130-645A-109784
C 3	24.2	30.6	64	19	US-11-130-645A-109784
C 4	24.2	30.6	64	19	US-11-130-645A-169416
C 5	24.2	30.6	64	19	US-11-130-645A-169416
C 6	22.4	28.4	63	19	US-11-130-645A-348741
C 7	22.4	28.4	63	19	US-11-130-645A-498699
C 8	22.4	28.4	64	19	US-11-130-645A-245318
C 9	21.6	27.3	64	19	US-11-130-645A-51361
C 10	21.6	27.3	64	19	US-11-130-645A-156960
C 11	21.6	27.3	64	19	US-11-130-645A-243478
C 12	21.6	27.3	64	19	US-11-130-645A-385098

12	21.6	27.3	64	19	US-11-130-645A-426292	Sequence 426292,
13	21.6	27.3	64	19	US-11-130-645A-641194	Sequence 641194,
14	21.6	27.3	64	19	US-11-130-645A-660220	Sequence 660220,
15	21.6	27.3	63	19	US-11-130-645A-90177	Sequence 90177, A
C 16	20.6	26.1	63	19	US-11-130-645A-121147	Sequence 121147,
C 17	20.6	26.1	64	19	US-11-130-645A-524994	Sequence 524994,
C 18	20.6	26.1	64	19	US-11-130-645A-538349	Sequence 538349,
C 19	20	25.3	32	11	US-10-536-560-38260	Sequence 38260, A
C 20	20	25.3	64	19	US-11-130-645A-85134	Sequence 85134, A
C 21	20	25.3	64	19	US-11-130-645A-89154	Sequence 89154, A
C 22	20	25.3	64	19	US-11-130-645A-126839	Sequence 126839,
C 23	19.8	25.1	32	11	US-10-536-560-133728	Sequence 133728,
C 24	19.8	25.1	32	11	US-10-536-560-189867	Sequence 189867,
C 25	19.8	25.1	62	19	US-11-130-645A-39117	Sequence 39117, A
C 26	19.8	25.1	64	19	US-11-130-645A-145738	Sequence 145738,
C 27	19.8	25.1	64	19	US-11-130-645A-295048	Sequence 295048,
C 28	19.8	25.1	64	19	US-11-130-645A-393179	Sequence 393179,
C 29	19.8	25.1	64	19	US-11-130-645A-433301	Sequence 433301,
C 30	19.8	25.1	64	19	US-11-130-645A-546370	Sequence 546370,
C 31	19.8	25.1	64	19	US-11-130-645A-626880	Sequence 626880,
C 32	19.6	24.8	59	19	US-11-130-645A-108583	Sequence 108583,
C 33	19.6	24.8	64	19	US-11-130-645A-50209	Sequence 50209, A
C 34	19.6	24.8	64	19	US-11-130-645A-71244	Sequence 71244, A
C 35	19.6	24.8	64	19	US-11-130-645A-102927	Sequence 102927,
C 36	19.6	24.8	64	19	US-11-130-645A-276984	Sequence 276984,
C 37	19.6	24.8	64	19	US-11-130-645A-282851	Sequence 282851,
C 38	19.6	24.8	64	19	US-11-130-645A-386537	Sequence 386537,
C 39	19.6	24.8	64	19	US-11-130-645A-395089	Sequence 395089,
C 40	19.6	24.8	64	19	US-11-130-645A-395200	Sequence 395200,
C 41	19.6	24.8	64	19	US-11-130-645A-426224	Sequence 426224,
C 42	19.6	24.8	64	19	US-11-130-645A-483135	Sequence 483135,
C 43	19.6	24.8	64	19	US-11-130-645A-601445	Sequence 601445,
C 44	19.6	24.8	64	19	US-11-130-645A-646153	Sequence 646153,
C 45	19.6	24.8	64	19	US-11-130-645A-720580	Sequence 720580,

## ALIGNMENTS

RESULT 1  
US-10-536-560-26233/c  
; Sequence 26233, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 06087.0300.PCUI3  
; CURRENT APPLICATION NUMBER: US/10/536.560  
; CURRENT FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 424571  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 26233  
; LENGTH: 32  
; TYPE: RNA  
; ORGANISM: Homo Sapiens  
US-10-536-560-26233

Query Match 40.5%; Score 32; DB 11; Length 32;  
Best Local Similarity 65.6%; Pred. No. 0.67;  
Matches 21; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 25 CUCUGGCCCCUUAUUGUACUUGCGGCUUGUA 56  
|:|||||:|||||:|||||:|||||:|||||:|  
Db 32 CTCTGGCCCCCTTATTGTCTACTTCGGCTCGTA 1

RESULT 2  
US-11-130-645A-109784/c  
; Sequence 109784, Application US/11130645A  
; Publication No. US20070050146A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwick, Itzhak

```

1  APPLICANT:  Amir, Avniel
2  APPLICANT:  Yael, Karov
3  APPLICANT:  Ranit, Aharonov
4  TITLE OF INVENTION:  Micornas and Uses Thereof
5  FILE REFERENCE:  06087.0202.CPUS13
6  CURRENT APPLICATION NUMBER:  US/11/130,645A
7  CURRENT FILING DATE:  2005-05-16
8  PRIOR APPLICATION NUMBER:  PCT/US05/16986
9  PRIOR FILING DATE:  2005-05-14
10 PRIOR APPLICATION NUMBER:  US 10/709,577
11 PRIOR FILING DATE:  2004-05-14
12 PRIOR APPLICATION NUMBER:  US 10/709,572
13 PRIOR FILING DATE:  2004-05-14
14 PRIOR APPLICATION NUMBER:  US 60/666,340
15 PRIOR FILING DATE:  2005-03-30
16 PRIOR APPLICATION NUMBER:  US 60/665,094
17 PRIOR FILING DATE:  2005-03-25
18 PRIOR APPLICATION NUMBER:  US 60/662,742
19 PRIOR FILING DATE:  2005-03-17
20 PRIOR APPLICATION NUMBER:  US 60/593,329
21 PRIOR FILING DATE:  2005-01-06
22 PRIOR APPLICATION NUMBER:  US 60/593,081
23 PRIOR FILING DATE:  2004-12-08
24 PRIOR APPLICATION NUMBER:  US 60/522,860
25 PRIOR FILING DATE:  2004-11-15
26 PRIOR APPLICATION NUMBER:  US 60/522,457
27 PRIOR FILING DATE:  2004-10-04
28 Remaining Prior Application data removed - See File Wrapper or PALM.
29 NUMBER OF SEQ ID NOS:  760616
30 SOFTWARE:  PatentIn version 3.3
31 SEQ ID NO 109784
32 LENGTH:  63
33 TYPE:  RNA
34 ORGANISM:  Homo sapiens
35 JS-11-130-645A-109784

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	Query Match	30.6%	Score 24.2	DB 19	Length 63
Best Local Similarity	37.8%	Pred. No. 3.3e+02			
Matches 17	Conservative 15	Mismatches 13	Indels 0	Gaps 0	
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Db	56	CTCCATCCCATCTCTACTCTCGGGTCCTTTGTCCCTGCCCT	12		

RESULT 3  
US-11-130-645A-22287/c  
; Sequence 22287, Application US/11130645A  
; Publication No. US20070050146A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Amir, Avniel  
; APPLICANT: Yael, Karov  
; APPLICANT: Ranit, Ahatonov  
; TITLE OF INVENTION: Micronovas and Uses Thereof  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130,645A  
; CURRENT FILING DATE: 2005-05-16  
; PRIOR APPLICATION NUMBER: PCT/US05/16986  
; PRIOR FILING DATE: 2005-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,577  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,572  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 60/666,340  
; PRIOR FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: US 60/665,094  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/662,742  
; PRIOR FILING DATE: 2005-03-17  
; PRIOR APPLICATION NUMBER: US 60/593,329  
; PRIOR FILING DATE: 2005-01-06  
; PRIOR APPLICATION NUMBER: US 60/593,081

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; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76016
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22287
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
; PS-11-130-645A-22287

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	Query Match	30.6%	Score 24.2;	DB 19;	Length 64;
	Best Local Similarity	37.8%;	Pred. No. 3.3e+02;		
	Matches 17;	Conservative	15;	Mismatches 13;	Indels 0; Gaps 0;
Qy	25	CUCUGGGCCCUUAAUUGUACUUCGGGCU	CGUAVUGUCUUCUCCUUU	69	
Db	59	CTCCATCCCATTCTCTTCTTGGGTCCTT	TGTGCCCTCCCTT	15	

RESULT 4  
US-11-130-645A-169416/c  
Sequence 169416, Application US/11130645A  
Publication No. US20070050146A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Itzhak  
APPLICANT: Amir, Avniel  
APPLICANT: Yael, Karov  
APPLICANT: Ranit, Aharonov  
TITLE OF INVENTION: Micronovas and Uses Thereof  
FILE REFERENCE: 06087.0202.CPUS13  
CURRENT APPLICATION NUMBER: US/11/130, 645A  
CURRENT FILING DATE: 2005-05-16  
PRIOR APPLICATION NUMBER: PCT/US05/16986  
PRIOR FILING DATE: 2005-05-14  
PRIOR APPLICATION NUMBER: US 10/709,577  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 10/709,572  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 60/666,340  
PRIOR FILING DATE: 2005-03-30  
PRIOR APPLICATION NUMBER: US 60/665,094  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/662,742  
PRIOR FILING DATE: 2005-03-17  
PRIOR APPLICATION NUMBER: US 60/593,329  
PRIOR FILING DATE: 2005-01-06  
PRIOR APPLICATION NUMBER: US 60/593,081  
PRIOR FILING DATE: 2004-12-08  
PRIOR APPLICATION NUMBER: US 60/522,860  
PRIOR FILING DATE: 2004-11-15  
PRIOR APPLICATION NUMBER: US 60/522,457  
PRIOR FILING DATE: 2004-10-04  
Remaining Prior Application data removed - See  
NUMBER OF SEQ ID NOS: 760616  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 169416  
LENGTH: 64  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-130-645A-169416

Query Match	30.6%	Score 24.2;	DB 19;	Length 64;
Best Local Similarity	37.8%;	Fred. No. 3.3e+02;		
Matches	17;	Conservative 15;	Mismatches 13;	Indels 0;
Gaps	0;			

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; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 498699
; LENGTH: 63
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-498699

Query Match      28.4%      Score 22.4; DB 19; Length 63;
Best Local Similarity 48.2%; Pred. No. 1.3e+03;
Matches 27; Conservative 8; Mismatches 21; Indels 0; Gaps:

Qy      2      GAGGGCGGGGAGAGACGAGCGGCGUCUGGCCCCUUAUUGUACUUCGGGCGUCGUAU 57
Db      56      GTGGGCGCTGGAGGCGTCAGCAGCACTGTGGCCCTCTGCATCACCCCTTGGGGCAGGTCT 1

RESULT 7
US-11-130-645A-245318/c
; Sequence 245318, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: Microtarns and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 245318
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-245318

Query Match      28.4%      Score 22.4; DB 19; Length 64;

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; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 426292
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-426292

Query Match          27.1%; Score 21.6; DB 19; Length 64;
Best Local Similarity 58.2%; Pred.No. 2.5e+03;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 27 CUGGCCCCUUAUUGACUUCUGGGCGUGUAUUGUCUCUCCUUC 70
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Db 14 CUGGCCCCUUCUGGGUUAUGAGCUGGAACUGUUCUACUUC 57

RESULT 13
US-11-130-645A-641194
; Sequence 641194, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17

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; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 641194
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-641194

Query Match      27.3%; Score 21.6; DB 19; Length 64;
Best Local Similarity 68.2%; Pred. No. 2.5e+03;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 27 CUGGCCCCUUAUUGUACUUCGGGCGUUAUUGUCUUCUUCUUC 70
DB 14 CUGGCCCCUUAUUGUAGGUGUUAUUGAGCUGGAAACUGUUAUUCUUC 57

RESULT 14
US-11-130-645A-660220
; Sequence 660220, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 660220
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-660220

Query Match      27.3%; Score 21.6; DB 19; Length 64;
Best Local Similarity 68.2%; Pred. No. 2.5e+03;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 27 CUGGCCCCUUAUUGUACUUCGGGCGUUAUUGUCUUCUUCUUC 70
DB 14 CUGGCCCCUUAUUGUAGGUGUUAUUGAGCUGGAAACUGUUAUUCUUC 57

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DB 14 CUGGCCCCUUAUUGUAGGUGUUAUUGAGCUGGAAACUGUUAUUCUUC 57

RESULT 15
US-11-130-645A-90177
; Sequence 90177, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 90177
; LENGTH: 65
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-90177

Query Match      27.3%; Score 21.6; DB 19; Length 65;
Best Local Similarity 68.2%; Pred. No. 2.5e+03;
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 27 CUGGCCCCUUAUUGUACUUCGGGCGUUAUUGUCUUCUUCUUC 70
DB 15 CUGGCCCCUUAUUGAGGUGUUAUUGAGCUGGAAACUGUUAUUCUUC 58

Search completed: June 19, 2007, 16:25:10
Job time : 2967 secs

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GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 14:05:10 ; Search time 2495 Seconds  
(without alignments)  
1964.425 Million cell updates/sec

Title: US-10-604-726A-5135

Perfect score: 79

Sequence: 1 ggagggcggggagagacga.....ucucuccuucgaccucc 79

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 624300

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: gb\_est6:.\*  
6: gb\_est7:.\*  
7: gb\_est8:.\*  
8: gb\_est9:.\*  
9: gb\_est10:.\*  
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19: gb\_est20:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.6	27.3	76	5	BX728792
2	20.6	26.1	76	12	EC019237
3	19.8	25.1	78	19	CT351516
4	19.6	24.8	71	17	CW020424
5	19.4	24.6	58	19	CR076775
6	19.4	24.6	71	13	DN441479
7	19.4	24.6	76	16	BZ381406
8	19.4	24.6	76	17	CW236987
9	19.4	24.6	78	11	H25883
10	19.4	24.6	78	12	EC034520
11	19.2	24.3	46	1	A1360975
12	19.2	24.3	50	7	AU105862
13	19.2	24.3	66	17	CW022621
14	19.2	24.3	78	18	DX045680

C	15	19.2	24.3	79	1	AI539851
	16	19	24.1	51	19	BX289701
	17	19	24.1	65	11	EC687830
C	18	19	24.1	78	10	CR587313
C	19	19	24.1	79	15	AZ605020
	20	18.8	23.8	46	1	AA569383
C	21	18.8	23.8	61	8	CB046583
	22	18.8	23.8	67	12	DY248960
C	23	18.8	23.8	73	8	CD945332
	24	18.8	23.8	78	3	BQ029975
	25	18.6	23.5	37	15	AZ769939
	26	18.6	23.5	48	15	AZ767626
C	27	18.6	23.5	73	1	AA912015
	28	18.6	23.5	73	12	EB988681
	29	18.6	23.5	79	12	EB783239
	30	18.4	23.3	50	7	AU103010
	31	18.4	23.3	50	7	AU103012
	32	18.4	23.3	69	12	EC054167
C	33	18.4	23.3	70	11	EC693412
	34	18.4	23.3	74	16	CC458134
	35	18.4	23.3	77	13	DR337378
C	36	18.2	23.0	32	17	CL300541
	37	18.2	23.0	50	7	AU102976
	38	18.2	23.0	52	15	AZ769999
	39	18.2	23.0	58	1	AI554529
C	40	18.2	23.0	63	8	CF297944
	41	18.2	23.0	73	19	ATH551807
	42	18.2	23.0	77	19	CR106056
C	43	18.2	23.0	79	12	EC459732
	44	18	22.8	64	15	AZ921047
C	45	18	22.8	65	19	DE108298

#### ALIGNMENTS

RESULT 1  
BX728792  
LOCUS  
DEFINITION BX728792 XGC-tadpole Xenopus tropicalis cdna clone TTPA036j08 5',  
mRNA sequence.  
ACCSSION BX728792  
VERSION BX728792.1 GI:38401533  
KEYWORDS EST.  
SOURCE Xenopus tropicalis (western clawed frog)  
ORGANISM Xenopus tropicalis  
REFERENCE 1 (bases 1 to 76)  
AUTHORS Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.  
TITLE Sanger Xenopus tropicalis EST project 2001 (11\_2003)  
JOURNAL Unpublished (2003)  
COMMENT Contact: Croning MDR  
Sanger Institute  
Hinnton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE ID: TTPA036j08.pikSP6  
Sequencing primer: SP6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Nigel Garrett.  
cDNA was oligo dT primed from sug of poly A+ RNA from tadpole  
embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with  
EcoRI at the 5' end and NotI at the 3' end.  
Vector: pCS107; Site 1: EcoRI; Site 2: NotI  
Host: Escherichia coli DH10B.  
location/Qualifiers  
1..76  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="TTPA036j08"



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/sex="male"  
/cell_type="Embryonic stem cell"
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/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pFLIP1"

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Query Match      24.8%; Score 19.6; DB 17; Length 71;
Best Local Similarity 52.0%; Pred. No. 8.7e+04;
Matches 26; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 1 GGGGGGGGGGAGAGACGAGCGGCGUCUGGCCCUAAUUGUACUUGCGG 50
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Db 1 GGGGGGGGGGGAACGAGCGGGGGCCCCCTTTTATACAGGGG 50

RESULT 5
LOCUS CR076775 58 bp DNA linear GSS 05-JUL-2004
DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and
            chromosome engineering clone MHP113c17, genomic survey sequence.
ACCESSION CR076775
VERSION GSS; genome survey sequence; MICE.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 58)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICE
FEATURES
    source
        1..58
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
            /clone="MHP113c17"
            /clone_lib="MHP"

ORIGIN
Query Match      24.6%; Score 19.4; DB 19; Length 59;
Best Local Similarity 75.9%; Pred. No. 1e+05;
Matches 22; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 GAGGGCGGGGAGAGACGAGCGGCGUCUGG 30
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 GAGGGCGGGGAGAGCGGGGGCGAGCACTGG 49

RESULT 6
LOCUS DN441479 71 bp mRNA linear EST 08-MAR-2005
DEFINITION LIB5338-102-A1-K2-G6 LIB5338 Canis familiaris cDNA clone
            CLN14241789, mRNA sequence.
ACCESSION DN441479
VERSION DN441479.1 GI:60637724
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 71)
AUTHORS Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
        Tel: 636 247 6855
        Email: nicholas.r.staten@pfizer.com.
        Location/Qualifiers

QY 14 GAGACGAGCGGCGUCUGGCCCUAAUUGUACUUGCGGCGUAGUUGUCUCC 66

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source
1..71
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CLN14241789"
/tissue_type="kidney"
/lab_host="DH10B"
/clone_lib="LIB5338"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; whole
organ"

ORIGIN
Query Match      24.6%; Score 19.4; DB 13; Length 71;
Best Local Similarity 45.3%; Pred. No. 1e+05;
Matches 24; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 5 GGGGGGGGAGAGACGAGCGGCGUCUGGCCCUAAUUGUACUUGCGGCGUAGU 57
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 17 GGGGGGAGCGGAGACCGCGGCCCGCCACCAATTGTTCTCTCGGTCTTCT 69

RESULT 7
LOCUS BZ381406 76 bp DNA linear GSS 26-NOV-2002
DEFINITION SALK_116666.43.10.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_116666.43.10.x, genomic
            survey sequence.
ACCESSION BZ381406
VERSION BZ381406.1 GI:25475317
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 76)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
        Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
        Salk Institute Genomic Analysis Laboratory (SIGNAL)
        The Salk Institute for Biological Studies
        10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
        Tel: 858 453 4100 x1752
        Fax: 858 558 6379
        Email: ecker@salk.edu
        This is single pass sequence recovered from the left border of
        TDNA. This sequence lies within an annotated exon of At5g61190.
        Class: TDNA tagged.
        Location/Qualifiers
            1..76
                /organism="Arabidopsis thaliana"
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                /note="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
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Best Local Similarity 37.7%; Pred. No. 1e+05;
Matches 20; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 14 GAGACGAGCGGCGUCUGGCCCUAAUUGUACUUGCGGCGUAGUUGUCUCC 66

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GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
1499.898 Million cell updates/sec

Title: US-10-604-726A-5136

Perfect score: 24

Sequence: 1 uauugucucuccuugccaccuc 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 2038054

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	15.6	65.0	24	2	AR010025 Sequence
C 3	15.6	65.0	24	2	AR034743 Sequence
C 4	15.6	65.0	24	2	AR034760 Sequence
C 5	15.6	65.0	24	2	124740 Sequence 3
C 6	15.6	65.0	24	2	124752 Sequence 15
C 7	15.2	63.3	21	2	AR877903 Sequence
C 8	15.2	63.3	22	2	AR877901 Sequence
C 9	14.4	60.0	18	2	AR072296 Sequence
C 10	14.4	60.0	18	2	126407 Sequence
C 11	14.4	60.0	20	2	AR877905 Sequence
C 12	14.2	59.2	21	2	128585 Sequence 38
C 13	14.2	59.2	21	2	158747 Sequence 38
C 14	14.2	59.2	25	2	AX649750 Sequence
C 15	14.2	59.2	25	2	AX649751 Sequence
C 16	14.2	59.2	25	2	AX649752 Sequence
C 17	14.2	59.2	25	2	AX649753 Sequence
C 18	14.2	59.2	25	2	AX649754 Sequence

C 19	14.2	59.2	25	2	AX649755 Sequence
C 20	14.2	59.2	25	2	AX649756 Sequence
C 21	14	58.3	24	2	A24320 LST3 Primer
C 22	14	58.3	24	2	AR010021 Sequence
C 23	14	58.3	24	2	AR034756 Sequence
C 24	14	58.3	24	2	124749 Sequence 12
C 25	13.8	57.5	17	2	AX648244 Sequence
C 26	13.8	57.5	20	2	BD268715 Inhibitor
C 27	13.8	57.5	20	2	CQ764854 Sequence
C 28	13.8	57.5	20	2	AR229112 Sequence
C 29	13.8	57.5	20	2	AR281375 Sequence
C 30	13.8	57.5	20	2	AR304584 Sequence
C 31	13.8	57.5	20	2	AR312823 Sequence
C 32	13.8	57.5	20	2	AR337580 Sequence
C 33	13.8	57.5	20	2	AR590429 Sequence
C 34	13.8	57.5	25	2	AX649748 Sequence
C 35	13.8	57.5	25	2	AX649749 Sequence
C 36	13.6	56.7	20	2	BD411373 Method fo
C 37	13.6	56.7	22	2	CS113604 Sequence
C 38	13.4	55.8	17	2	AR072297 Sequence
C 39	13.4	55.8	17	2	DD023799 YEAST-BAS
C 40	13.4	55.8	17	2	I26408 Sequence 10
C 41	13.4	55.8	17	2	AX469671 Sequence
C 42	13.4	55.8	18	2	BD345059 Antisense
C 43	13.4	55.8	18	2	CS177232 Sequence
C 44	13.4	55.8	18	2	AR882372 Sequence
C 45	13.4	55.8	18	2	AX191825 Sequence

#### ALIGNMENTS

RESULT 1	AR010008/c	AR010008	Sequence 20 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR010008	Sequence 20 from patent US 5756684.					
DEFINITION	AR010008						
ACCESSION	AR010008.1	GI:3968813					
VERSION	AR010008.1	GI:3968813					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 24)						
AUTHORS	Johnson, E.M. and Bergemann, A.D.						
TITLE	Cloning and expression of PUR protein						
JOURNAL	Patent: US 5756684-A 20 26-MAY-1998;						
FEATURES	Location/Qualifiers						
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Qy 3 UUGUCUCUCUUGCCACCUC 24  
Db 23 TTTCCTCCCTCCACCCTC 2

RESULT 2	AR010025	AR010025	Sequence 38 from patent US 5756684.	24 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR010025	Sequence 38 from patent US 5756684.					
DEFINITION	AR010025						
ACCESSION	AR010025						
VERSION	AR010025.1	GI:3968830					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 24)						
AUTHORS	Johnson, E.M. and Bergemann, A.D.						

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TITLE      Cloning and expression of PUR protein
JOURNAL    Patent: US 5756684-A 38 26-MAY-1998;
FEATURES   Location/Qualifiers
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LOCUS
DEFINITION      Sequence 20 from patent US 5869622.
ACCESSION      AR034743
VERSION        AR034743.1 GI:5950348
KEYWORDS
SOURCE
ORGANISM
REFERENCE      1 (bases 1 to 24)
AUTHORS      Johnson,E.M. and Bergemann,A.D.
TITLE      Monoclonal antibodies to the pur protein
JOURNAL      Patent: US 5869622-A 20 09-FEB-1999;
FEATURES   Location/Qualifiers
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QY      3 UUGUCUCUCUUGGCCACCUC 24
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Db      2 TTTTCTCTCCCTCCACCCTC 23

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LOCUS
DEFINITION      Sequence 38 from patent US 5869622.
ACCESSION      AR034760
VERSION        AR034760.1 GI:5950365
KEYWORDS
SOURCE
ORGANISM
REFERENCE      1 (bases 1 to 24)
AUTHORS      Johnson,E.M. and Bergemann,A.D.
TITLE      Monoclonal antibodies to the pur protein
JOURNAL      Patent: US 5869622-A 38 09-FEB-1999;
FEATURES   Location/Qualifiers
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TITLE      Cloning and expression of PUR protein
JOURNAL    Patent: US 5756684-A 38 26-MAY-1998;
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Db      2 TTTTCTCTCCCTCCACCCTC 23

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LOCUS
DEFINITION      Sequence 3 from patent US 5545551.
ACCESSION      I24740
VERSION        I24740.1 GI:1604610
KEYWORDS
SOURCE
ORGANISM
REFERENCE      1 (bases 1 to 24)
AUTHORS      Johnson,E.M. and Bergmann,A.D.
TITLE      Cloning and expression of pur protein
JOURNAL      Patent: US 5545551-A 3 13-AUG-1996;
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Db      23 TTTTCTCTCTCCCTCCACCCTC 2

RESULT 6
I24752      24 bp      DNA      linear      PAT 07-OCT-1996
LOCUS
DEFINITION      Sequence 15 from patent US 5545551.
ACCESSION      I24752
VERSION        I24752.1 GI:1604622
KEYWORDS
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ORGANISM
REFERENCE      1 (bases 1 to 24)
AUTHORS      Johnson,E.M. and Bergmann,A.D.
TITLE      Cloning and expression of pur protein
JOURNAL      Patent: US 5545551-A 15 13-AUG-1996;
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Best Local Similarity 50.0%; Pred. No. 2e+04;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      3 UUGUCUCUCUUGGCCACCUC 24
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Db      23 TTTTCTCTCTCCCTCCACCCTC 2

RESULT 7
AR877903/c      21 bp      DNA      linear      PAT 11-AUG-2006
LOCUS
DEFINITION      Sequence 2144 from patent US 7045289.
ACCESSION      AR877903
VERSION        AR877903.1 GI:111975391
KEYWORDS
SOURCE
ORGANISM
REFERENCE      1 (bases 1 to 21)
AUTHORS      Allawi,H., Bartholomay,C.T., Chehak,L., Curtis,M.L., Eis,P.S.,
           Hall,J.G., Ip,H.S., Kaiser,M., Kwiatkowski,R.W. Jr., Lukowiak,A.A.,
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REFERENCE  
AUTHORS  
TITLE

Best Local Similarity 56.2%; Pred. No. 7.1e+04;  
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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Db 19 GTCTCTCTTTGCCA 4

RESULT 12  
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ACCESSION 128585  
VERSION 128585.1 GI:1819361  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Watanabe,K.A., Ren,W.-Y. and Weil,R.  
TITLE Complementary DNA and toxins  
JOURNAL Patent: US 5571937-A 38 05-NOV-1996;  
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Db 19 TTTTATCTCTCTTCTCC 1

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LOCUS 158747/c  
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ACCESSION 158747  
VERSION 158747.1 GI:2477985  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Watanabe,K.A., Ren,W.-Y. and Weil,R.  
TITLE Complementary DNA and toxins  
JOURNAL Patent: US 5652350-A 38 29-JUL-1997;  
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ACCESSION AX649750  
VERSION AX649750.1 GI:29152568  
KEYWORDS

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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.  
1  
REFERENCE Gu,Y.  
AUTHORS Human sodium-hydrogen exchanger like protein 1  
TITLE Patent: EP 1273660-A 1590 08-JAN-2003;  
JOURNAL Aeomica, Inc. (US)  
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Db 25 ACTGTCTCTCCATCCCA 7

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ACCESSION AX649751  
VERSION AX649751.1 GI:29152569  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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REFERENCE Gu,Y.  
AUTHORS Human sodium-hydrogen exchanger like protein 1  
TITLE Patent: EP 1273660-A 1591 08-JAN-2003;  
JOURNAL Aeomica, Inc. (US)  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.  
1  
REFERENCE Gu,Y.  
AUTHORS Human sodium-hydrogen exchanger like protein 1  
TITLE Patent: EP 1273660-A 1590 08-JAN-2003;  
JOURNAL Aeomica, Inc. (US)  
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QY 2 AUUGUCUCUUCGCCA 20  
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Search completed: June 19, 2007, 13:51:04  
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ORGANISM Homo sapiens  
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REFERENCE Gu,Y.  
AUTHORS Human sodium-hydrogen exchanger like protein 1  
TITLE Patent: EP 1273660-A 1590 08-JAN-2003;  
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QY 2 AUUGUCUCUUCGCCA 20  
Db 24 ACTGTCTCTCCATCCCA 6

Search completed: June 19, 2007, 13:51:04  
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GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

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Perfect score: 24  
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- 16: Geneseqn2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 4	15.6	65.0	24	2	AAT99274 Human PUR
C 5	15.6	65.0	24	2	AAV31726 Nucleotid
C 6	15.6	65.0	24	2	AAV31731 Nucleotid
C 7	15.6	65.0	24	2	AAV31731 Nucleotid
C 8	15.6	65.0	24	2	AAV31731 Nucleotid
C 9	15.6	65.0	25	15	AAE94315 3' primer
C 10	15.2	63.3	21	7	ADI94591 Murine IF
C 11	15.2	63.3	22	7	ADI94589 Murine IF
C 12	14.4	60.0	18	2	AAQ65826 Type II p
C 13	14.4	60.0	20	7	ADI94593 Murine IF
C 14	14.4	60.0	23	2	AAQ85989 S.tuberos
C 15	14.2	59.2	21	2	AAQ56946 HIV-1 pro
C 16	14.2	59.2	21	15	AEFI3105 Human mut
C 17	14.2	59.2	25	10	ADC05103 Human Na/

C 18	14.2	59.2	25	10	ADC05104 Human Na/
C 19	14.2	59.2	25	10	ADC05109 Human Na/
C 20	14.2	59.2	25	10	ADC05105 Human Na/
C 21	14.2	59.2	25	10	ADC05108 Human Na/
C 22	14.2	59.2	25	10	ADC05106 Human Na/
C 23	14.2	59.2	25	10	ADC05107 Human Na/
C 24	14	58.3	24	2	AAQ38850 Sequence
C 25	14	58.3	24	2	AAQ44802 Oligonucle
C 26	14	58.3	24	2	AAT99270 Human PUR
C 27	14	58.3	24	2	AAV31727 Nucleotid
C 28	14	58.3	24	2	AAV31727 Nucleotid
C 29	14	58.3	24	5	AAH48099 Phytocbro
C 30	14	58.3	24	14	AEC26021 Human all
C 31	14	58.3	24	14	AEC26021 Human all
C 32	14	58.3	25	9	ACK16088 Human mic
C 33	13.8	57.5	17	10	ADC03597 Human Na/
C 34	13.8	57.5	20	2	AAQ4034 PCR prime
C 35	13.8	57.5	20	8	ABX04519 Human adi
C 36	13.8	57.5	20	10	ADC01938 Human zsi
C 37	13.8	57.5	20	10	AAQ59884 ZC13641 o
C 38	13.8	57.5	20	10	ADFI18008 Human zsi
C 39	13.8	57.5	20	10	ACD02558 Novel hum
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C 41	13.8	57.5	21	12	ADM72676 Human TAS
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C 44	13.8	57.5	25	9	ACI92741 Human mic
C 45	13.8	57.5	25	10	ADC05102 Human Na/

## ALIGNMENTS

RESULT 1

AAD21686/C

ID AAD21686 standard; DNA; 24 BP.

XX

AC AAD21686;

XX 28-JAN-2002 (first entry)

XX Imperfect direct repeat #1 of human RPGR exon ORF15 repetitive sequence.

DE Human; mutation; retinitis pigmentosa GTPase regulator; RPGR; genotyping;

XX open reading frame; ORF; X-linked retinitis pigmentosa; XLRP;

XX gene therapy; screening; forensic analysis; ds.

XX Homo sapiens.

OS WO200177380-A2.

XX 18-OCT-2001.

XX 10-APR-2001; 2001WO-GB001622.

XX 10-APR-2000; 2000GB-00008801.

XX (MEDI-) MEDICAL RES COUNCIL.

XX Wright A;

XX WPI; 2001-663057/76.

XX Diagnosing disease or predisposition to disease, associated with disease causing mutations in retinitis pigmentosa GTPase regulator gene by genotyping ORF15 of the gene, and determining presence of mutations.

XX Disclosure; Fig 4E; 100pp; English.

XX The present invention relates to a method for diagnosing disease or predisposition to a disease, associated with a disease causing mutations in a retinitis pigmentosa GTPase regulator (RPGR) gene involves genotyping a RPGR gene, and determining whether the genotype comprises a



DT 15-APR-1998 (first entry)  
XX Human PUR-alpha gene probe MR0700.  
XX  
DE  
XX  
KW PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;  
KW cancer; probe; hybridisation.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX US5672479-A.  
XX  
XX  
XX 30-SEP-1997.  
XX  
XX 07-JUN-1995; 95US-00486421.  
XX  
XX 28-AUG-1992; 92US-00938189.  
XX  
XX 02-FEB-1993; 93US-00014943.  
XX  
XX 06-JUN-1995; 95US-00470911.  
XX  
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
XX  
XX Bergemann AD, Johnson EM;  
XX  
XX WPI; 1997-488859/45.  
XX  
XX Assays for PUR protein ligands or modulators - using immobilised PUR  
XX protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.  
XX  
XX Example; Col 26; 64pp; English.  
XX  
XX The probes AAT99270-T99277 were used to screen for positive clones  
XX containing a 467 bp Sau3AI fragment of the human c-myc upstream region  
XX cloned into pUC19. Isolated sequences were then used as probes to screen  
XX an expression library for sequences encoding the PUR protein. The PUR  
XX sequence can be used to identify chemical or biological compounds that  
XX bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may  
XX be used to treat hyperproliferative diseases such as cancer  
XX  
XX Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 4.8e+03;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 3 UUGUCUCUCUUGCCACCTC 24  
DB 2 TTTTCTCTCCCTCCACCACTC 23  
RESULT 5  
AAV31726/c  
ID AAV31726 standard; DNA; 24 BP.  
XX  
XX AAV31726;  
XX  
XX 24-SEP-1998 (first entry)  
XX  
XX Nucleotide sequence of the PUR element.  
XX  
XX PUR-alpha gene; inhibition; viral infection; cancer; PUR element;  
XX hyperproliferative disease; ss.  
XX  
XX Homo sapiens.  
XX  
XX US5756684-A.  
XX  
XX 26-MAY-1998.  
XX  
XX 06-JUN-1995; 95US-00470911.  
XX  
XX 28-AUG-1992; 92US-00938189.  
XX  
XX 02-FEB-1993; 93US-00014943.  
XX  
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
XX  
XX Bergemann AD, Johnson EM;  
XX  
XX WPI; 1998-321632/28.  
XX  
XX PUR protein and its fragments - that inhibit PUR protein binding to PUR  
XX element or other proteins.  
XX  
XX Example 6.1.1; Col 27; 63pp; English.  
XX  
XX This is the nucleotide sequence of an oligonucleotide used in the method  
XX of the invention, involving the use of the PUR protein and its fragments,  
XX which inhibit PUR protein binding to PUR element or other proteins.  
XX Inhibitors of PUR activity may be useful for treating viral infections  
XX and hyperproliferative diseases such as cancer  
XX  
XX Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 4.8e+03;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 3 UUGUCUCUCUUGCCACCTC 24  
DB 2 TTTTCTCTCCCTCCACCACTC 23

XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
XX  
XX Bergemann AD, Johnson EM;  
XX  
XX WPI; 1998-321632/28.  
XX  
XX PUR protein and its fragments - that inhibit PUR protein binding to PUR  
XX element or other proteins.  
XX  
XX Disclosure; Col 12; 63pp; English.  
XX  
XX This is the nucleotide sequence of the PUR element used in the method of  
XX the invention, involving the use of the PUR protein and its fragments,  
XX which inhibit PUR protein binding to PUR element or other proteins.  
XX Inhibitors of PUR activity may be useful for treating viral infections  
XX and hyperproliferative diseases such as cancer  
XX  
XX Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 4.8e+03;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 3 UUGUCUCUCUUGCCACCTC 24  
DB 23 TTTTCTCTCCCTCCACCACTC 2  
RESULT 6  
AAV31731  
ID AAV31731 standard; DNA; 24 BP.  
XX  
XX AAV31731;  
XX  
XX 24-SEP-1998 (first entry)  
XX  
XX Nucleotide sequence of the oligonucleotide MR0700.  
XX  
XX PUR-alpha gene; inhibition; viral infection; cancer; PUR element;  
XX hyperproliferative disease; ss.  
XX  
XX Synthetic.  
XX  
XX US5756684-A.  
XX  
XX 26-MAY-1998.  
XX  
XX 06-JUN-1995; 95US-00470911.  
XX  
XX 28-AUG-1992; 92US-00938189.  
XX  
XX 02-FEB-1993; 93US-00014943.  
XX  
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
XX  
XX Bergemann AD, Johnson EM;  
XX  
XX WPI; 1998-321632/28.  
XX  
XX PUR protein and its fragments - that inhibit PUR protein binding to PUR  
XX element or other proteins.  
XX  
XX Example 6.1.1; Col 27; 63pp; English.  
XX  
XX This is the nucleotide sequence of an oligonucleotide used in the method  
XX of the invention, involving the use of the PUR protein and its fragments,  
XX which inhibit PUR protein binding to PUR element or other proteins.  
XX Inhibitors of PUR activity may be useful for treating viral infections  
XX and hyperproliferative diseases such as cancer  
XX  
XX Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 4.8e+03;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 3 UUGUCUCUCUUGCCACCTC 24  
DB 23 TTTTCTCTCCCTCCACCACTC 2

XX	Oligonucleotide MR0700 used in PUR identification/characterisation.
XX	DE
XX	PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
XX	monoclonal antibody; identification; characterisation; ss.
XX	Synthetic.
OS	Homo sapiens.
XX	US5869622-A.
XX	09-FEB-1999.
XX	07-JUN-1995; 95US-00486809.
XX	28-AUG-1992; 92US-00938189.
XX	02-FEB-1993; 93US-00014943.
XX	06-JUN-1995; 95US-00470911.
XX	(MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX	Bergemann AD, Johnson EM;
XX	WPI; 1999-152881/13.
XX	Monoclonal antibody specific for PUR protein - useful for treating
XX	cancer.
XX	Example; Col 27; 64pp; English.
XX	The present invention describes a monoclonal antibody that specifically
XX	binds to an epitope of the PUR protein. Antibodies that bind to the PUR
XX	protein and neutralise PUR activity may be used to treat
XX	hyperproliferative diseases such as cancer. PUR antibodies may be used
XX	diagnostically to detect aberrant expression of the PUR protein and/or
XX	mutations in the PUR gene. The present sequence represents an
XX	oligonucleotide used in the identification and characterisation of the
XX	PUR protein and its sequence element PUR repeat, in an example from the
XX	present invention
XX	Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
XX	Query Match 65.0%; Score 15.6; DB 2; Length 24;
XX	Best Local Similarity 50.0%; Pred. No. 4.8e+03;
XX	Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY	3 UUGUCUCUCUUGGCCACUC 24
DB	:::::
DB	2 TTCTCTCCCTCCACCACTC 23
XX	RESULT 9
XX	AEE94315/c
XX	ID AEE94315 standard; DNA; 25 BP.
XX	AEE94315;
XX	AC
XX	23-FEB-2006 (first entry)
XX	3' primer for PCR of DNase I treated OLIG2 chromatin.
XX	DE
XX	chromatin; DNA hybridization; DNA amplification; DNA microarray;
XX	diagnosis; ss; primer; PCR; OLIG2.
XX	Homo sapiens.
XX	WO2005118873-A2.
XX	15-DEC-2005.
XX	31-MAY-2005; 2005WO-US019150.
XX	28-MAY-2004; 2004US-0575478P.

XX (CEMI-) CEMINES INC.  
 XX Neuman T;  
 XX WPI; 2006-047578/05.  
 XX  
 PT Detecting open chromatin comprises determining hybridization of the  
 PT capture probe to the treated- and untreated-sample amplification  
 PT products.  
 XX Example 1; Page 37; 43pp; English.  
 XX  
 CC The new invention relates to detecting open chromatin in genomic DNA by  
 CC determining the hybridization of a capture probe to a treated sample  
 CC amplification products and the untreated sample amplification products.  
 CC Specifically, the method comprises preparing a chromatin sample from  
 CC cells, the chromatin sample comprising genomic DNA segments or genomic  
 CC DNA with one or more open chromatin sites; treating a first portion of  
 CC the chromatin sample with an open chromatin DNA cleaving agent to produce  
 CC fragments; performing a first amplification reaction using the fragments  
 CC as a substrate, to produce treated-sample amplification products;  
 CC performing a second amplification reaction using a second portion of the  
 CC chromatin sample, where the second portion is not treated with the open  
 CC chromatin DNA cleaving agent, to produce untreated-sample amplification  
 CC products; incubating the treated-sample amplification products and the  
 CC untreated-sample amplification products with a capture probe; and  
 CC determining the hybridization of the capture probe to the products, where  
 CC the untreated-sample amplification products hybridize to the capture  
 CC probe, and where reduced hybridization of the capture probe to the  
 CC treated-sample amplification products as compared to the hybridization of  
 CC the capture probe to the untreated-sample amplification products  
 CC indicates the presence of open chromatin in the genomic DNA. Also given  
 CC is a chromatin state profiling array, for detecting the presence of open  
 CC chromatin in genomic DNA. The methods and chromatin state profiling array  
 CC are useful for detecting open chromatin in genomic DNA, used in  
 CC diagnostic and prognostic methods, and are useful for monitoring  
 CC treatment and evaluating the response of cells and patients to candidate  
 CC or established therapeutic agents. The present sequence is a 3' reverse  
 CC primer for one-sided PCR amplification of DNase I treated chromatin  
 CC fragments, deposited on a chromatin profiling array.  
 XX  
 SQ Sequence 25 BP; 13 A; 0 C; 11 G; 1 T; 0 U; 0 Other;  
 Query Match 65.0%; Score 15.6; DB 15; Length 25;  
 Best Local Similarity 40.9%; Pred. No. 4.8e+03;  
 Matches 9; Conservative 9; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 AUGUCUCUCUUUGCCACCU 23  
 Db 22 ATTCTCTCTTTTCTCTCT 1  
 RESULT 10  
 ADI94591/c  
 ID ADI94591 standard; DNA; 21 BP.  
 XX  
 AC ADI94591;  
 XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 DE Murine IFN-gamma associated probe SEQ ID 2144.  
 XX  
 KW functional domain; nucleic acid cleavage assay; nuclease; polymerase;  
 KW detection; microorganism; RNA genome; hepatitis C;  
 KW human immunodeficiency virus; ss; probe.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200190337-A2.  
 XX  
 PD 29-NOV-2001.  
 XX

PF 24-MAY-2001; 2001WO-US017086.  
 XX  
 PR 24-MAY-2000; 2000US-00577304.  
 PR 11-JAN-2001; 2001US-00758282.  
 PR 24-MAY-2001; 2001US-00864426.  
 PR 24-MAY-2001; 2001US-00864636.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Allawi H, Bartholomay CT, Chehak L, Curtis ML, Eis PS, Hall JG;  
 PI IP HS, Kaiser M, Kwiatkowski RW, Lukowiak AA, Lyamichev V, Ma W;  
 PI Olson-Munoz MC, Olson SM, Schaefer JJ, Skrzypczynski Z, Takova TY;  
 PI Vedvik KL, Lyamichev NE, Neri BP;  
 XX  
 DR WPI; 2002-083110/11.  
 XX  
 CC Composition comprising enzyme which comprises heterologous functional  
 CC domain that provides altered functionality in nucleic acid cleavage  
 CC assay, useful for cleaving nucleic acid, and detecting presence of RNA  
 CC target.  
 XX  
 PS Claim 95; SEQ ID NO 2144; 1266pp; English.  
 XX  
 CC This invention describes a novel composition comprising an enzyme which  
 CC contains a heterologous functional domain that provides altered  
 CC functionality in a nucleic acid cleavage assay. The enzyme comprises a 5'  
 CC nuclease, preferably a thermostable 5' nuclease, or a polymerase which is  
 CC altered in sequence related to a naturally occurring sequence of a  
 CC polymerase such that it exhibits reduced DNA synthetic activity from that  
 CC of the naturally occurring polymerase. Preferably the polymerase is a  
 CC thermostable polymerase from a Thermus species such as T. aquaticus, T.  
 CC flavus, T. thermophilus, T. filiformis or T. scotoductus. The enzyme  
 CC comprises a heterologous functional domain, an amino acid sequence that  
 CC provides an improved substrate binding activity in the nucleic acid  
 CC cleavage assay and an amino acid sequence that provides improved  
 CC background specificity in the nucleic acid cleavage assay. The invasive  
 CC cleavage structure comprises a RNA target nucleic acid (a cytochrome  
 CC P450, or cytokine RNA). Cleavage of the invasive cleavage structure  
 CC generates an non-target cleavage product, which is then detected by  
 CC detecting fluorescence, mass or fluorescence energy transfer or by  
 CC detecting radioactivity luminescence, phosphorescence, fluorescence  
 CC polarisation or charge. The enzyme is useful for cleaving a nucleic acid  
 CC which involves exposing a sample (a cell lysate) comprising substrate  
 CC nucleic acid to the enzyme which produces at least one detectable  
 CC cleavage product. The enzyme is employed for detecting target DNAs and  
 CC RNAs comprising wild-type and mutant alleles of genes including genes  
 CC from humans, other animal or plants that are or may be associated with  
 CC disease or other conditions. In addition, the enzymes may be useful for  
 CC detecting and identifying strains of microorganisms including bacteria,  
 CC fungi, protozoa, ciliates and viruses, preferably detecting and  
 CC identifying viruses having RNA genomes, such as hepatitis C and human  
 CC immunodeficiency virus.  
 XX  
 SQ Sequence 21 BP; 9 A; 3 C; 8 G; 1 T; 0 U; 0 Other;  
 Query Match 63.3%; Score 15.2; DB 7; Length 21;  
 Best Local Similarity 50.0%; Pred. No. 7e+03; 3; Indels 0; Gaps 0;  
 Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 GUCUCUCUUUGCCACCU 24  
 Db 20 GTCTCTCTTTTGGCAGTTC 1  
 RESULT 11  
 ADI94589/c  
 ID ADI94589 standard; DNA; 22 BP.  
 XX  
 AC ADI94589;  
 XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 DE Murine IFN-gamma associated probe SEQ ID 2142.

XX functional domain; nucleic acid cleavage assay; nuclease; polymerase;  
 KW detection; microorganism; RNA genome; hepatitis C;  
 KW human immunodeficiency virus; ss; probe.  
 XX Mus musculus.  
 OS  
 PN W0200190337-A2.  
 XX  
 XX 29-NOV-2001.  
 PD  
 XX 24-MAY-2001; 2001WO-US017086.  
 XX  
 XX 24-MAY-2000; 2000US-00577304.  
 PR  
 PR 11-JAN-2001; 2001US-00758282.  
 PR  
 PR 24-MAY-2001; 2001US-00864426.  
 PR  
 PR 24-MAY-2001; 2001US-00864636.  
 XX  
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 PA  
 XX Allawi H, Bartholomay CT, Chehak L, Curtis ML, Eis PS, Hall JG;  
 PI Ip HS, Kaiser M, Kwiatkowski RW, Lukowski AA, Lymanichev V, Ma W;  
 PI Olson-Munoz MC, Olson SM, Schaefer JU, Skrzypczynski Z, Takova TY;  
 PI Vedvik KL, Lymanichev NE, Neri BP;  
 XX  
 XX WPI; 2002-083110/11.  
 DR  
 XX Composition comprising enzyme which comprises heterologous functional  
 XX domain that provides altered functionality in nucleic acid cleavage  
 XX assay, useful for cleaving nucleic acid, and detecting presence of RNA  
 XX target.  
 XX  
 XX Claim 95; SEQ ID NO 2142; 1266pp; English.  
 PS  
 XX This invention describes a novel composition comprising an enzyme which  
 XX contains a heterologous functional domain that provides altered  
 XX functionality in a nucleic acid cleavage assay. The enzyme comprises a 5'  
 XX nuclease, preferably a thermostable 5' nuclease, or a polymerase which is  
 XX altered in sequence related to a naturally occurring sequence of a  
 XX polymerase such that it exhibits reduced DNA synthetic activity from that  
 XX of the naturally occurring polymerase. Preferably the polymerase is a  
 XX thermostable polymerase from a Thermus species such as T. aquaticus, T.  
 XX flavus, T. thermophilus, T. filiformis or T. scotoductus. The enzyme  
 XX comprises a heterologous functional domain, an amino acid sequence that  
 XX provides an improved substrate binding activity in the nucleic acid  
 XX cleavage assay and an amino acid sequence that provides improved  
 XX background specificity in the nucleic acid cleavage assay. The invasive  
 XX cleavage structure comprises a RNA target nucleic acid (a cytochrome  
 XX P450, or cytokine RNA). Cleavage of the invasive cleavage structure  
 XX generates a non-target cleavage product, which is then detected by  
 XX detecting fluorescence, mass or fluorescence energy transfer or by  
 XX detecting radioactivity luminescence, phosphorescence, fluorescence  
 XX polarisation or charge. The enzyme is useful for cleaving a nucleic acid  
 XX which involves exposing a sample (a cell lysate) comprising substrate  
 XX nucleic acid to the enzyme which produces at least one detectable  
 XX cleavage product. The enzyme is employed for detecting target DNAs and  
 XX RNAs comprising wild-type and mutant alleles of genes including genes  
 XX from humans, other animal or plants that are or may be associated with  
 XX disease or other conditions. In addition, the enzymes may be useful for  
 XX detecting and identifying strains of microorganisms including bacteria,  
 XX fungi, protozoa, ciliates and viruses, preferably detecting and  
 XX identifying viruses having RNA genomes, such as hepatitis C and human  
 XX immunodeficiency virus.  
 XX  
 XX Sequence 22 BP; 9 A; 3 C; 9 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 63.3%; Score 15.2; DB 7; Length 22;  
 Best Local Similarity 50.0%; Pred. No. 7.1e+03;  
 Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
 OY 5 GUCUCUCCUUGCCACUCC 24  
 Db 21 GTCCTCTCTTTCGCCAGTTC 2

RESULT 12  
 AAQ65826  
 ID AAQ65826 standard; DNA; 18 BP.  
 XX  
 AC AAQ65826;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 20-DEC-1994 (first entry)  
 DT  
 XX Type II procollagen sequencing primer 96.  
 DE  
 XX Type II procollagen; COL2A1; amplification; primer;  
 KW polymerase chain reaction; PCR; osteoarthritis; cartilage; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX W09411532-A1.  
 PN  
 XX 26-MAY-1994.  
 PD  
 XX 12-NOV-1993; 93WO-US010964.  
 PF  
 XX 13-NOV-1992; 92US-00977284.  
 PR  
 XX (UVE-) UNIV JEFFERSON THOMAS.  
 XX  
 XX Prockop DJ, Ala-Kotko L, Williams CJ, Ritvaniemi P, Baldwin C;  
 PI Hopkinson I, Ahmad NN;  
 PI  
 XX WPI; 1994-183530/22.  
 DR  
 XX Detecting genetic pre-disposition to osteoarthritis - and other diseases  
 XX involving mutation in cartilage protein genes, by amplification and  
 XX analysis of DNA and comparison with standards.  
 XX  
 XX Claim 18; Page 26; 112pp; English.  
 PS  
 XX Claim 18 claims primers for use in detecting mutations in a mammalian  
 XX gene for a structural protein of cartilage comprising a sequence  
 XX identified in Table 1 (Page 18-31). Table 1 includes 179 primer sequences  
 XX (see AAQ65728-065906). The following details are given for primer 96:  
 XX Region/exon: 31 Direction: sense Primer position: 12824 (Updated on 25-  
 XX MAR-2003 to correct PN field.)  
 CC  
 XX Sequence 18 BP; 1 A; 10 C; 1 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 60.0%; Score 14.4; DB 2; Length 18;  
 Best Local Similarity 62.5%; Pred. No. 1.5e+04;  
 Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 OY 9 CUUUUUUCCACUCC 24  
 Db 3 CTCCTTTCGCCACCTC 18  
 RESULT 13  
 ADI94593/c  
 ID ADI94593 standard; DNA; 20 BP.  
 XX  
 AC ADI94593;  
 XX  
 XX 04-NOV-2004 (first entry)  
 DT  
 XX Murine IFN-gamma associated probe SEQ ID 2146.  
 DE  
 XX functional domain; nucleic acid cleavage assay; nuclease; polymerase;  
 KW detection; microorganism; RNA genome; hepatitis C;  
 KW human immunodeficiency virus; ss; probe.  
 XX  
 XX Mus musculus.  
 OS  
 XX



PN WO200190337-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US017086.  
XX  
XX 24-MAY-2000; 2000US-00577304.  
PR 11-JAN-2001; 2001US-00758282.  
PR 24-MAY-2001; 2001US-00864426.  
PR 24-MAY-2001; 2001US-00864636.  
XX  
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
PA  
XX Allawi H, Bartholomay CT, Chehak L, Curtis ML, Eis PS, Hall JG;  
PI Ip HS, Kaiser M, Kwiatkowski RW, Lukowiak AA, Lyamichev V, Ma W;  
PI Olson-Munoz MC, Olson SM, Schaefer JJ, Skrzypczynski Z, Takova TY,  
PI Vedvik KL, Lyamichev NE, Neri BP;  
XX WPI; 2002-083110/11.  
DR  
XX Composition comprising enzyme which comprises heterologous functional  
XX domain that provides altered functionality in nucleic acid cleavage  
PT assay, useful for cleaving nucleic acid, and detecting presence of RNA  
PT target.  
XX  
XX Claim 95; SEQ ID NO 2146; 1266pp; English.  
XX  
XX This invention describes a novel composition comprising an enzyme which  
XX contains a heterologous functional domain that provides altered  
XX functionality in a nucleic acid cleavage assay. The enzyme comprises a 5'  
XX nuclease, preferably a thermostable 5' nuclease, or a polymerase which is  
XX altered in sequence related to a naturally occurring sequence of a  
XX polymerase such that it exhibits reduced DNA synthetic activity from that  
XX of the naturally occurring polymerase. Preferably the polymerase is a  
XX thermostable polymerase from a Thermus species such as T. aquaticus, T.  
XX flavus, T. thermophilus, T. filiformis or T. scotoductus. The enzyme  
XX comprises a heterologous functional domain, an amino acid sequence that  
XX provides an improved substrate binding activity in the nucleic acid  
XX cleavage assay and an amino acid sequence that provides improved  
XX background specificity in the nucleic acid cleavage assay. The invasive  
XX cleavage structure comprises a RNA target nucleic acid (a cytochrome  
XX P450, or cytokine RNA). Cleavage of the invasive cleavage structure  
XX generates a non-target cleavage product, which is then detected by  
XX detecting fluorescence, mass or fluorescence energy transfer or by  
XX detecting radioactivity luminescence, phosphorescence, fluorescence  
XX polarisation or charge. The enzyme is useful for cleaving a nucleic acid  
XX which involves exposing a sample (a cell lysate) comprising substrate  
XX nucleic acid to the enzyme which produces at least one detectable  
XX cleavage product. The enzyme is employed for detecting target DNAs and  
XX RNAs comprising wild-type and mutant alleles of genes including genes  
XX from humans, other animal or plants that are or may be associated with  
XX disease or other conditions. In addition, the enzymes may be useful for  
XX detecting and identifying strains of microorganisms including bacteria,  
XX fungi, protozoa, ciliates and viruses, preferably detecting and  
XX identifying viruses having RNA genomes, such as hepatitis C and human  
XX immunodeficiency virus.  
XX  
XX Sequence 20 BP; 9 A; 3 C; 7 G; 1 T; 0 U; 0 Other;  
XX  
Query Match 60.0%; Score 14.4; DB 7; Length 20;  
Best Local Similarity 56.2%; Pred. No. 1.5e+04;  
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 5 GUCUCUCCUUUGCCCA 20  
DB 19 GTCTCTCTTTTGCCA 4  
RESULT 14  
AAQ85989/c  
ID AAQ85989 standard; DNA; 23 BP.  
XX  
AC AAQ85989;

XX  
DT 25-MAR-2003 (revised)  
DT 12-OCT-1995 (first entry)  
XX  
XX S. tuberosum PFK probe PFK23.  
XX  
XX ATP-dependent fructose-6-phosphate 1-phosphotransferase enzyme; plant;  
KW potato; Solanum tuberosum; rice; Oryza sativa; maize; Zea mays; radish;  
KW Raphanus sativus; Flaveria brownii; primer; expression vector; probe;  
KW Agrobacterium tumefaciens; sugar; storage; temperature; ss.  
OS Synthetic.  
XX  
XX WO9505457-A1.  
XX  
XX 23-FEB-1995.  
XX  
XX 16-AUG-1994; 94WO-JP001352.  
XX  
XX 19-AUG-1993; 93JP-00226454.  
XX  
XX (NISR) JAPAN TOBACCO INC.  
XX  
XX Hiroyoshi T, Mine T, Kasaoka K, Tyson HR, Page MJA;  
XX WPI; 1995-098757/13.  
XX  
XX DNA coding for fructose-6-phosphate 1-phosphotransferase - of plant  
XX origin, for prodn. of transformant plant cells with altered sugar  
XX content.  
XX  
XX Example 7; Page 15; 79pp; Japanese.  
XX  
XX The sequence of the probe PFK23 derived from a 60 bp amplified fragment  
XX encoding an N-terminal peptide (AAR71610) from the novel potato (Solanum  
XX tuberosum) ATP-dependent fructose-6-phosphate 1-phosphotransferase enzyme  
XX (EC 2.7.1.11; PFK). The probe was used to obtain 11 clones of the PFK  
XX gene. These clones, amplified by PCR using the primers (AAQ85990-3),  
XX ligated into the plasmid pBluescript SKII(-). The full length gene  
XX (AAQ85982) was used to generate the expression vector pPFK(35S) which was  
XX transformed into plants via Agrobacterium tumefaciens. Transformed plants  
XX expressing the enzyme can be used to produce varieties that have altered  
XX sugar content on storage at low temperatures. (Updated on 25-MAR-2003 to  
XX correct PN field.)  
XX  
XX Sequence 23 BP; 9 A; 0 C; 9 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 60.0%; Score 14.4; DB 2; Length 23;  
Best Local Similarity 56.2%; Pred. No. 1.6e+04;  
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 8 UCUCUUUUGCCACCU 23  
DB 20 TCTCTCTTTTCCACCT 5  
RESULT 15  
AAQ56946/c  
ID AAQ56946 standard; DNA; 21 BP.  
XX  
XX AAQ56946;  
XX  
XX 16-OCT-2003 (revised)  
DT 15-JUL-1999 (first entry)  
XX  
XX HIV-1 proviral DNA fragment 29.  
XX  
XX DNA-targeting conjugate; anticancer drug; viral DNA-cleaving agent;  
KW viral DNA-binding agent; solid support; primer; ss.  
XX  
XX Human immunodeficiency virus 1.  
XX  
XX WO9531434-A1.



GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:53:27 ; Search time 256 Seconds  
(without alignments)  
175.760 Million cell updates/sec

Title: US-10-604-726A-5136

Perfect score: 24

Sequence: 1 uauugucucuccuucgcaccuc 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 960512

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H COMB.seq.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq.\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.6	65.0	24	2	US-08-014-943A-3
C 2	15.6	65.0	24	2	US-08-014-943A-15
C 3	15.6	65.0	24	2	US-08-486-421-20
C 4	15.6	65.0	24	2	US-08-486-421-38
C 5	15.6	65.0	24	2	US-08-470-911-20
C 6	15.6	65.0	24	2	US-08-470-911-38
C 7	15.6	65.0	24	2	US-08-486-809-20
C 8	15.6	65.0	24	2	US-08-486-809-38
C 9	14.4	60.0	18	2	US-07-977-284A-99
C 10	14.4	60.0	18	2	US-08-256-426B-99
C 11	14.2	59.2	21	2	US-08-242-664-38
C 12	14.2	59.2	21	2	US-08-484-138-38
C 13	14.2	59.2	21	7	PCT-US95-06379-38
C 14	14	58.3	24	2	US-08-014-943A-12
C 15	14	58.3	24	2	US-08-486-421-34
C 16	14	58.3	24	2	US-08-470-911-34
C 17	14	58.3	25	3	US-08-486-809-34
C 18	14	58.3	25	3	US-09-396-196G-81941
C 19	13.8	57.5	20	3	US-09-118-408-10
C 20	13.8	57.5	20	3	US-09-506-855-10
C 21	13.8	57.5	20	3	US-09-911-176B-10
C 22	13.8	57.5	20	3	US-09-619-740-10
C 23	13.8	57.5	20	3	US-09-198-452A-3360

C 24	13.8	57.5	20	3	US-09-506-852-10	Sequence 10, Appl
C 25	13.8	57.5	20	3	US-10-392-706-10	Sequence 10, Appl
C 26	13.6	56.7	25	3	US-09-396-196G-64399	Sequence 64399, A
C 27	13.6	56.7	25	3	US-09-396-196G-119671	Sequence 119671, A
C 28	13.4	55.8	17	2	US-07-977-284A-100	Sequence 100, Appl
C 29	13.4	55.8	17	2	US-08-256-426B-100	Sequence 100, Appl
C 30	13.4	55.8	24	3	US-08-445-463B-56	Sequence 56, Appl
C 31	13.4	55.8	24	3	US-08-445-463B-57	Sequence 57, Appl
C 32	13.4	55.8	24	3	US-08-445-464C-56	Sequence 56, Appl
C 33	13.4	55.8	24	3	US-08-445-464C-57	Sequence 57, Appl
C 34	13.4	55.8	24	3	US-08-044-857D-56	Sequence 56, Appl
C 35	13.4	55.8	24	3	US-08-044-857D-57	Sequence 57, Appl
C 36	13.4	55.8	24	7	PCT-US94-03437-56	Sequence 56, Appl
C 37	13.4	55.8	24	7	PCT-US94-03437-57	Sequence 57, Appl
C 38	13.4	55.8	25	3	US-09-543-771B-365	Sequence 365, Appl
C 39	13.4	55.8	25	3	US-09-543-771B-365	Sequence 365, Appl
C 40	13.4	55.8	25	3	US-09-396-196G-14417	Sequence 14417, A
C 41	13.4	55.8	25	3	US-09-396-196G-14428	Sequence 14428, A
C 42	13.4	55.8	25	3	US-09-396-196G-57430	Sequence 57430, A
C 43	13.4	55.8	25	3	US-09-396-196G-117149	Sequence 117149, A
C 44	13.2	55.0	20	3	US-09-265-630-15	Sequence 15, Appl
C 45	13.2	55.0	21	3	US-08-983-605-322	Sequence 322, Appl

ALIGNMENTS

RESULT 1  
US-08-014-943A-3/C  
; Sequence 3, Application US/08014943A  
; Patent No. 5545551  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Edward M.  
; APPLICANT: Bergemann, Andrew D.  
; TITLE OF INVENTION: Cloning And Expression Of PUR Protein  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/014,943A  
; FILING DATE: 02/FEB/1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 6923-033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-014-943A-3

Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 6.4e+02;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCUCCUUGCCACCUC 24  
Db 23 TTTTCTCTCCCTCCACCCTC 2

## RESULT 2

US-08-014-943A-15  
; Sequence 15, Application US/08014943A  
; Patent No. 5545551  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Edward M.  
; APPLICANT: Bergemann, Andrew D.  
; TITLE OF INVENTION: Cloning And Expression Of PUR Protein  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/014,943A  
; FILING DATE: 02/FEB/1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 6923-033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-014-943A-15

Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 6.4e+02;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCUCCUUGCCACCUC 24  
Db 2 TTTTCTCTCCCTCCACCCTC 23

## RESULT 3

US-08-486-421-20/c  
; Sequence 20, Application US/08486421  
; Patent No. 5672479  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Edward M.  
; APPLICANT: Bergemann, Andrew D.  
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,421  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/470,911  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 6923-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-486-421-20

Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 6.4e+02;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 UUGUCUCUCUCCUUGCCACCUC 24  
Db 23 TTTTCTCTCCCTCCACCCTC 2

## RESULT 4

US-08-486-421-38  
; Sequence 38, Application US/08486421  
; Patent No. 5672479  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Edward M.  
; APPLICANT: Bergemann, Andrew D.  
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,421  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/470,911  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 6923-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-486-421-38

Query Match 65.0%; Score 15.6; DB 2; Length 24;

Best Local Similarity 50.0%; Pred. No. 6.4e+02;

Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Oy 3 UUGUCUCUCCUUUGCCACCUC 24

Db 2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 5

US-08-470-911-20/c

; Sequence 20, Application US/08470911

; Patent No. 5756684

; GENERAL INFORMATION:

; APPLICANT: Johnson, Edward M.

; APPLICANT: Bergemann, Andrew D.

; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,911

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 6923-053

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

US-08-470-911-20

Query Match 65.0%; Score 15.6; DB 2; Length 24;

Best Local Similarity 50.0%; Pred. No. 6.4e+02;

Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Oy 3 UUGUCUCUCCUUUGCCACCUC 24

Db 23 TTTTCTCTCCCTCCACCACCTC 2

RESULT 6

US-08-470-911-38

; Sequence 38, Application US/08470911

; Patent No. 5756684

; GENERAL INFORMATION:

; APPLICANT: Johnson, Edward M.

; APPLICANT: Bergemann, Andrew D.

; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,911

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 6923-053

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-470-911-38

Query Match

Best Local Similarity 50.0%; Score 15.6; DB 2; Length 24;

Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Oy 3 UUGUCUCUCCUUUGCCACCUC 24

Db 2 TTTTCTCTCCCTCCACCACCTC 23

RESULT 7

US-08-486-809-20/c

; Sequence 20, Application US/08486809

; Patent No. 5869622

; GENERAL INFORMATION:

; APPLICANT: Johnson, Edward M.

; APPLICANT: Bergemann, Andrew D.

; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,809

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/470,911  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-486-809-20

Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. NO. 6.4e+02;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCCUUUGCCACCC 24  
Db 23 TTTTCTCTCCCTCCACCCCTC 2

RESULT 8  
US-08-486-809-38  
Sequence 38, Application US/08486809  
Patent No. 5869622  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,809  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,911  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-486-809-38

Query Match 65.0%; Score 15.6; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. NO. 6.4e+02;  
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCCUUUGCCACCC 24  
Db 2 TTTTCTCTCCCTCCACCCCTC 23

RESULT 9  
US-07-977-284A-99  
Sequence 99, Application US/07977284A  
Patent No. 5558988  
GENERAL INFORMATION:  
APPLICANT: Prockop, Darwin J.  
APPLICANT: Ala-Kokko, Leena  
APPLICANT: Williams, Charlene J.  
APPLICANT: Ritvaniemi, Pertti  
APPLICANT: Baldwin, Clinton  
APPLICANT: Hopkinson, Ian  
APPLICANT: Ahmad, Nilofer Nina  
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC  
TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS  
NUMBER OF SEQUENCES: 261  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/977,284A  
FILING DATE: 13-NOV-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TLU-0697  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
ANTI-SENSE: NO  
US-07-977-284A-99

Query Match 60.0%; Score 14.4; DB 2; Length 18;  
Best Local Similarity 62.5%; Pred. NO. 2.1e+03;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CUCCUUUGCCACCC 24  
Db 3 CTCCTTTCCACCCCTC 18

RESULT 10  
US-08-256-426B-99  
Sequence 99, Application US/08256426B  
Patent No. 5948611  
GENERAL INFORMATION:

APPLICANT: Prockop, Darwin J.  
APPLICANT: Ala-Kokko, Leena  
APPLICANT: Williams, Charlene J.  
APPLICANT: Ritvianemi, Pertti  
APPLICANT: Baldwin, Clinton  
APPLICANT: Hopkinson, Ian  
APPLICANT: Ahmad, Nilofer Nina  
TITLE OF INVENTION: Methods of Detecting A Genetic  
NUMBER OF SEQUENCES: 293  
CORRESPONDENCE ADDRESS:  
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORDPERFECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,426B  
FILING DATE: 03-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10964  
FILING DATE: 12-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,284  
FILING DATE: 13-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark Deluca  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-1082  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
ANTI-SENSE: NO  
US-08-256-426B-99

Query Match 60.0%; Score 14.4; DB 2; Length 18;  
Best Local Similarity 62.5%; Pred. No. 2.1e+03;  
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 9 CUUUUUGCCACUC 24  
Db 3 CTCCTTCCACCTC 18

RESULT 11  
US-08-242-664-38/c  
Sequence 38, Application US/08242664  
Patent No. 5571937  
GENERAL INFORMATION:  
APPLICANT: Watanabe, Kyoichi A.  
APPLICANT: Ren, Wu-Yun  
APPLICANT: Weil, Roger  
TITLE OF INVENTION: Complementary DNA and Toxins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44Mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/242,664  
FILING DATE: May 12, 1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 44683  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-242-664-38

Query Match 59.2%; Score 14.2; DB 2; Length 21;  
Best Local Similarity 36.8%; Pred. No. 2.7e+03;  
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUGUCUCUUCUUGGCC 19  
Db 19 TTTTATCTCTCTTTCTCC 1

RESULT 12  
US-08-484-138-38/c  
Sequence 38, Application US/08484138  
Patent No. 5652350  
GENERAL INFORMATION:  
APPLICANT: Watanabe, Kyoichi A.  
APPLICANT: Ren, Wu-Yun  
APPLICANT: Weil, Roger  
TITLE OF INVENTION: Complementary DNA and Toxins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44Mb  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,138  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
US-08-484-138-38

Query Match      59.2%; Score 14.2; DB 2; Length 21;
Best Local Similarity 36.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCUCCUUGGCC 19
Db 19 TTTTATCTCTCCTTTCTCC 1

RESULT 13
PCT-US95-06379-38/c
; Sequence 38, Application PC/TUS9506379
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; APPLICANT: Weil, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06379
; FILING DATE: May 13, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-38

Query Match      59.2%; Score 14.2; DB 7; Length 21;
Best Local Similarity 36.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCUCCUUGGCC 19
Db 19 TTTTATCTCTCCTTTCTCC 1

RESULT 14
US-08-014-943A-12/c
; Sequence 12, Application US/08014943A
; Patent No. 5545551
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: Cloning And Expression Of PUR Protein
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
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; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,943A
; FILING DATE: 02/FEB/1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-014-943A-12

Query Match      58.3%; Score 14; DB 2; Length 24;
Best Local Similarity 40.9%; Pred. No. 3.4e+03;
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 3 UUGUCUCUCUCCUUGCCACCC 24
Db 23 TTTTCTCTTTTCCACCCCTC 2

RESULT 15
US-08-486-421-34/c
; Sequence 34, Application US/08486421
; Patent No. 5672479
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,421
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-486-421-34

Query Match      58.3%; Score 14; DB 2; Length 24;
Best Local Similarity 40.9%; Pred. No. 3.4e+03;
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy      3 UUGUCUCUCUUCGCGCACCTC 24
Db      23 TTTCTCTTTTCCACCACTC 2

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Search completed: June 19, 2007, 13:10:06  
Job time : 255.5 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:01:01 ; Search time 1262 Seconds  
(without alignments)  
233.679 Million cell updates/sec

Title: US-10-604-726a-5136

Perfect score: 24

Sequence: 1 uauugucucuccuugccacc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 22906428

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA Main:\*

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- 2: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
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- 9: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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c 2	16	66.7	25	9	US-10-719-900-980988
c 3	16	66.7	25	10	US-10-956-157-42579
c 4	16	66.7	25	10	US-10-956-157-88871
c 5	16	66.7	25	10	US-10-956-157-88877
c 6	16	66.7	25	13	US-11-060-756-47774
c 7	16	66.7	25	13	US-11-060-756-47788
c 8	15.8	65.8	24	11	US-10-310-914A-205339
c 9	15.8	65.8	25	16	US-11-136-527-276878
c 10	15.8	65.8	25	16	US-11-136-527-276903
c 11	15.6	65.0	25	9	US-10-719-900-678730
c 12	15.6	65.0	25	13	US-11-036-317-35846
c 13	15.4	64.2	20	11	US-10-310-914A-498782
c 14	15.4	64.2	25	10	US-10-956-157-21624
c 15	15.4	64.2	25	10	US-10-956-157-21630
c 16	15.4	64.2	25	10	US-10-956-157-21634
c 17	15.4	64.2	25	10	US-10-956-157-21637

c 18	15.2	63.3	21	3	US-09-864-636A-2144	Sequence 2144, Ap
c 19	15.2	63.3	21	3	US-09-864-636A-2144	Sequence 2144, Ap
c 20	15.2	63.3	21	7	US-10-084-839-2144	Sequence 2144, Ap
c 21	15.2	63.3	22	3	US-09-864-636A-2142	Sequence 2142, Ap
c 22	15.2	63.3	22	3	US-09-864-636A-2142	Sequence 2142, Ap
c 23	15.2	63.3	22	7	US-10-084-839-2142	Sequence 2142, Ap
c 24	15	62.5	19	14	US-11-083-784-661177	Sequence 661177,
c 25	15	62.5	19	15	US-11-101-244-661177	Sequence 661177,
c 26	15	62.5	25	10	US-10-956-157-42396	Sequence 42396, A
c 27	15	62.5	25	10	US-10-956-157-42570	Sequence 42570, A
c 28	15	62.5	25	10	US-10-956-157-43354	Sequence 43354, A
c 29	15	62.5	25	10	US-10-956-157-43356	Sequence 43356, A
c 30	15	62.5	25	10	US-10-956-157-43359	Sequence 43359, A
c 31	15	62.5	25	10	US-10-956-157-88872	Sequence 88872, A
c 32	15	62.5	25	13	US-11-060-756-47765	Sequence 47765, A
c 33	15	62.5	25	15	US-11-121-849-524825	Sequence 524825,
c 34	15	62.5	25	16	US-11-136-527-116930	Sequence 116930,
c 35	14.8	61.7	20	11	US-10-310-914A-949541	Sequence 949541,
c 36	14.8	61.7	21	11	US-10-310-914A-426363	Sequence 426363,
c 37	14.8	61.7	24	11	US-10-310-914A-67315	Sequence 67315, A
c 38	14.8	61.7	24	11	US-10-310-914A-144888	Sequence 144888,
c 39	14.8	61.7	24	11	US-10-310-914A-550631	Sequence 550631,
c 40	14.8	61.7	25	8	US-10-719-956-695018	Sequence 695018,
c 41	14.8	61.7	25	11	US-10-933-982-217334	Sequence 217334,
c 42	14.8	61.7	25	13	US-11-036-317-720298	Sequence 720298,
c 43	14.8	61.7	25	15	US-11-121-849-538357	Sequence 538357,
c 44	14.8	61.7	25	16	US-11-136-527-276882	Sequence 276882,
c 45	14.6	60.8	21	11	US-10-310-914A-1070230	Sequence 1070230,

#### ALIGNMENTS

#### RESULT 1

US-11-136-527-336045/c

; Sequence 336045, Application US/11136527

; Publication No. US20050287570A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 336045

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Probe

US-11-136-527-336045

Query Match 67.5%; Score 16.2; DB 16; Length 25;

Best Local Similarity 52.4%; Pred. No. 3.7e+03;

Matches 11; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AUUGUCUCUCUUGCCACC 22

Db 25 ATTGCTTCGTTGCCACC 5

#### RESULT 2

US-10-719-900-980988

; Sequence 980988, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1



FILE REFERENCE: AM101083 (031896-042000)  
CURRENT APPLICATION NUMBER: US/11/060,756  
CURRENT FILING DATE: 2005-02-18  
NUMBER OF SEQ ID NOS: 303284  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 47788  
LENGTH: 25  
TYPE: DNA  
ORGANISM: probe  
US-11-060-756-47788

Query Match 66.7%; Score 16; DB 13; Length 25;  
Best Local Similarity 45.8%; Pred. No. 4.5e+03;  
Matches 11; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCUCCUUGCCACCUC 24  
Db 25 TATCTCCCTCCCTTCACATC 2

## RESULT 8

US-10-310-914A-205339  
Sequence 205339, Application US/10310914A  
Publication No. US20050003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvazat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 205339

LENGTH: 24

TYPE: RNA

ORGANISM: Human

US-10-310-914A-205339

Query Match 65.8%; Score 15.8; DB 11; Length 24;  
Best Local Similarity 89.5%; Pred. No. 5.5e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AUGGUCUCUCUUGGCCA 20  
Db 5 AUGGUCUCUCUUGGCCA 23

## RESULT 9

US-11-136-527-276878  
Sequence 276878, Application US/11136527  
Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PatentIn version 3.2

SEQ ID NO 276878

LENGTH: 25

TYPE: DNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Probe

US-11-136-527-276878

Query Match 65.8%; Score 15.8; DB 16; Length 25;

Best Local Similarity 47.4%; Pred. No. 5.5e+03;  
Matches 9; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AUGGUCUCUCUUGGCCA 20  
Db 6 ATTGCTGCTCCTTTGGCCA 24

## RESULT 10

US-11-136-527-276903  
Sequence 276903, Application US/11136527  
Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PatentIn version 3.2

SEQ ID NO 276903

LENGTH: 25

TYPE: DNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Probe

US-11-136-527-276903

Query Match 65.8%; Score 15.8; DB 16; Length 25;  
Best Local Similarity 47.4%; Pred. No. 5.5e+03;  
Matches 9; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AUGGUCUCUCUUGGCCA 20  
Db 2 ATTGCTGCTCCTTTGGCCA 20

## RESULT 11

US-10-719-900-678730  
Sequence 678730, Application US/10719900  
Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 678730

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-10-719-900-678730

Query Match 65.0%; Score 15.6; DB 9; Length 25;  
Best Local Similarity 45.5%; Pred. No. 6.7e+03;  
Matches 10; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCUUGGCCACC 22  
Db 2 TATTGCTCAGCTTTAGTCACC 23

## RESULT 12

US-11-036-317-35846  
Sequence 35846, Application US/11036317  
Publication No. US20050214823A1

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; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 91174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 35846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-35846

Query Match      65.0%; Score 15.6; DB 13; Length 25;
Best Local Similarity 40.9%; Pred. No. 6.7e+03;
Matches 9; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 2 AUUGUCUCUCCUUGCCACCU 23
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Db 2 ATTCTGCTCTTTGGCTACCT 23
   |||:|:|:|:|:|:|:|:|:|

RESULT 13
US-10-310-914A-498782
; Sequence 498782, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 498782
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-498782

Query Match      64.2%; Score 15.4; DB 11; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 UCUCUCUCCUCCACC 22
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Db 3 UCUCUCUCCUCCCCC 19
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RESULT 14
US-10-956-157-21624/c
; Sequence 21624, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence

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US-10-956-157-21624

Query Match      64.2%; Score 15.4; DB 10; Length 25;
Best Local Similarity 47.1%; Pred. No. 8.2e+03;
Matches 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

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   |||:|:|:|:|:|:|:|
Db 23 ATTGTCTCTCTTCTC 7
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RESULT 15
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; Sequence 21630, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21630
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; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-21630

Query Match      64.2%; Score 15.4; DB 10; Length 25;
Best Local Similarity 47.1%; Pred. No. 8.2e+03;
Matches 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 2 AUUGUCUCUCCUUGCC 18
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Db 22 ATTGTCTCTCTTCTC 6
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Search completed: June 19, 2007, 16:27:50
Job time : 1264 secs

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GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:01:51 ; Search time 610 Seconds  
(without alignments)  
405.912 Million cell u

**Title:** US-10-604-726A-5136

Perfect score: 24  
Sequence: 1 uauuqucucuccuuucqccaccuc 24

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Total number of hits satisfying chosen parameters: 17957554

Minimum DB seq length: 0

Maximum DB seq length: 25

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Database : Published Applications NA New: \*\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	66.7	25	11	US-10-956-160-171431	Sequence 171431, A
2	15	62.5	19	10	US-10-714-333A-661177	Sequence 661177, A
3	15	62.5	19	17	US-11-093-832-661177	Sequence 661177, A
4	15	62.5	25	11	US-10-956-160-13205	Sequence 13205, A
5	15	62.5	25	11	US-10-956-160-25233	Sequence 25233, A
6	14.8	61.7	19	8	US-10-709-691B-215725	Sequence 215725, A
7	14.8	61.7	19	8	US-10-709-691B-2187318	Sequence 2187318, A
8	14.6	60.8	25	14	US-11-217-529-33285	Sequence 33285, A
9	14.4	60.0	19	10	US-10-714-333A-928822	Sequence 928822, A
10	14.4	60.0	19	10	US-10-714-333A-1077569	Sequence 1077569, A
11	14.4	60.0	19	10	US-10-714-333A-1245669	Sequence 1245669, A

C 12	14.4	60.0	19	10	US-10-714-333A-1245759	Sequence 1245759,
C 13	14.4	60.0	19	17	US-11-093-832-528822	Sequence 528822,
C 14	14.4	60.0	19	17	US-11-093-832-1077569	Sequence 1077569,
C 15	14.4	60.0	19	17	US-11-093-832-1245669	Sequence 1245669,
C 16	14.4	60.0	19	17	US-11-093-832-1245759	Sequence 1245759,
C 17	14.2	59.2	19	8	US-10-703-691B-2484540	Sequence 2484540,
C 18	14.2	59.2	19	9	US-10-703-691B-439600	Sequence 439600,
C 19	14.2	59.2	19	10	US-10-714-333A-792768	Sequence 792768,
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C 32	14.2	59.2	25	15	US-11-348-413-247873	Sequence 247873,
C 33	14.2	59.2	25	15	US-11-348-413-247874	Sequence 247874,
C 34	14.2	59.2	25	15	US-11-348-413-247875	Sequence 247875,
C 35	14.2	59.2	25	15	US-11-348-413-247876	Sequence 247876,
C 36	14.2	59.2	25	15	US-11-348-413-485166	Sequence 485166,
C 37	14.2	59.2	25	15	US-11-348-413-485167	Sequence 485167,
C 38	14.2	59.2	25	15	US-11-348-413-485168	Sequence 485168,
C 39	14.2	59.2	25	15	US-11-348-413-485634	Sequence 485634,
C 40	14.2	59.2	25	15	US-11-348-413-485635	Sequence 485635,
C 41	14.2	59.2	25	15	US-11-348-413-689385	Sequence 689385,
C 42	14.2	59.2	25	15	US-11-348-413-861056	Sequence 861056,
C 43	14.2	59.2	25	15	US-11-348-413-861057	Sequence 861057,
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## ALIGNMENTS

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; Sequence 171431, Application US/10956160
; Publication No. US2007000989A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR
; TITLE OF INVENTION: MODELS OF INFLAMMATO
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 171431
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-171431

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Query Match          66.7%; Score 16; DB 11; Length 25;
Best Local Similarity 41.7%; Pred. No. 2.9e+03;
Matches 10; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY      1  UAUUGUCUCUCCUUUUGCCGACCUC  24
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Db      1  TGTAGTCTCTCCCTTGACTACCTC  24

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; Sequence 661177, Application US/10714333A
; Publication No. US20070031844A1
; GENERAL INFORMATION:

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; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 661177
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; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-714-333A-661177

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Query Match 62.5%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 UAUGUCUCUCUCCUUU 15
Db 5 UAUGUCUCUCUCCUUU 19

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RESULT 3
US-11-093-832-661177
; Sequence 661177, Application US/11093832
; Publication No. US20070039072A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/093,832
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 661177
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-093-832-661177

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Query Match 62.5%; Score 15; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 UAUGUCUCUCUCCUUU 15
Db 5 UAUGUCUCUCUCCUUU 19

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RESULT 4
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; Sequence 13205, Application US/10956160
; Publication No. US20070009899A1

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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13205
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-10-956-160-13205

```

```

Query Match 62.5%; Score 15; DB 11; Length 25;
Best Local Similarity 47.8%; Pred. No. 8.2e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy 2 AUUGUCUCUCUCCUUGGCCACCU 24
Db 1 ATTGGCTCTGAATTAGCACCTC 23

```

```

RESULT 5
US-10-956-160-25233/c
; Sequence 25233, Application US/10956160
; Publication No. US20070009899A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25233
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-10-956-160-25233

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Query Match 62.5%; Score 15; DB 11; Length 25;
Best Local Similarity 43.5%; Pred. No. 8.2e+03;
Matches 10; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

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Qy 1 UAUGUCUCUCUCCUUGGCCACCU 23
Db 23 TCTGGTCTCTCTCTGGCTCTCT 1

```

```

RESULT 6
US-10-709-691B-2175725/c
; Sequence 2175725, Application US/10709691B
; Publication No. US20070031843A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Avniel, Amir
; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial
; TITLE OF INVENTION: and Bacterial Associated Oligonucleotides and Uses Thereof
; FILE REFERENCE: EIS23
; CURRENT APPLICATION NUMBER: US/10/709,691B
; CURRENT FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 4254815
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2175725
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Streptococcus pneumoniae R6

```

## US-10-709-691B-2175725

Query Match 61.7%; Score 14.8; DB 8; Length 19;  
Best Local Similarity 38.9%; Pred. No. 9.8e+03;  
Matches 7; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUCGC 18  
Db 19 TATTTTCTCCTTCGC 2

## RESULT 7

US-10-709-691B-2187318/c  
; Sequence 2187318, Application US/10709691B  
; Publication No. US20070031843A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Avniel, Amir  
; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
; FILE REFERENCE: Efs23  
; CURRENT APPLICATION NUMBER: US/10/709,691B  
; CURRENT FILING DATE: 2004-05-24  
; NUMBER OF SEQ ID NOS: 4254815  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2187318  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Streptococcus pneumoniae R6

## US-10-709-691B-2187318

Query Match 61.7%; Score 14.8; DB 8; Length 19;  
Best Local Similarity 38.9%; Pred. No. 9.8e+03;  
Matches 7; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUCGC 18  
Db 18 TATTTTCTCCTTCGC 1

## RESULT 8

US-11-217-529-33285  
; Sequence 33285, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 33285  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus

## US-11-217-529-33285

Query Match 60.8%; Score 14.6; DB 14; Length 25;  
Best Local Similarity 42.9%; Pred. No. 1.2e+04;  
Matches 9; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UGUCUCUCCUUCGCCACCU 23  
Db 4 TTGTCTCTTCATTGGACACCT 24

## RESULT 9

US-10-714-333A-928822/c  
; Sequence 928822, Application US/10714333A  
; Publication No. US20070031844A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/10/714,333A  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 928822  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

## US-10-714-333A-928822

Query Match 60.0%; Score 14.4; DB 10; Length 19;  
Best Local Similarity 37.5%; Pred. No. 1.5e+04;  
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUC 16  
Db 16 TATGTTCCTCCTTC 1

## RESULT 10

US-10-714-333A-1077569  
; Sequence 1077569, Application US/10714333A  
; Publication No. US20070031844A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/10/714,333A  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1077569  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens

## US-10-714-333A-1077569

Query Match 60.0%; Score 14.4; DB 10; Length 19;  
Best Local Similarity 37.5%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUC 16  
Db 3 UAUGUCUCUCCUUC 18



## RESULT 11

US-10-714-333A-1245669/c  
; Sequence 1245669, Application US/10714333A  
; Publication No. US20070031844A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/10/714,333A  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1245669  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-714-333A-1245669

Query Match 60.0%; Score 14.4; DB 10; Length 19;  
Best Local Similarity 37.5%; Pred. No. 1.5e+04;  
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUC 16  
:|::|::|::|::|::|  
Db 16 TATTCTCTCTCTTC 1

## RESULT 12

US-10-714-333A-1245759/c  
; Sequence 1245759, Application US/10714333A  
; Publication No. US20070031844A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/10/714,333A  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1245759  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-714-333A-1245759

Query Match 60.0%; Score 14.4; DB 10; Length 19;  
Best Local Similarity 37.5%; Pred. No. 1.5e+04;  
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUC 16  
:|::|::|::|::|::|  
Db 18 TATTCTCTCTCTTC 3

## RESULT 13

US-11-093-832-928822/c  
; Sequence 928822, Application US/11093832  
; Publication No. US20070039072A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/093,832  
; CURRENT FILING DATE: 2005-03-29  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 928822  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-093-832-928822

Query Match 60.0%; Score 14.4; DB 17; Length 19;  
Best Local Similarity 37.5%; Pred. No. 1.5e+04;  
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUC 16  
:|::|::|::|::|::|  
Db 16 TATTGTTCTCTTC 1

## RESULT 14

US-11-093-832-1077569  
; Sequence 1077569, Application US/11093832  
; Publication No. US20070039072A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/093,832  
; CURRENT FILING DATE: 2005-03-29  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1077569  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-093-832-1077569

Query Match 60.0%; Score 14.4; DB 17; Length 19;  
Best Local Similarity 93.8%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCCUUC 16  
|||||||

Db 3 UAUGUCUCUCCUUC 18

RESULT 15

US-11-093-832-1245669/c  
 ; Sequence 1245669, Application US/11093832  
 ; Publication No. US20070039072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmacon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/093,832  
 ; CURRENT FILING DATE: 2005-03-29  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1245669  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-11-093-832-1245669

Query Match 60.0%; Score 14.4; DB 17; Length 19;  
 Best Local Similarity 37.5%; Pred. No. 1.5e+04;  
 Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1 UAUGUCUCUCCUUC 16  
 :|::|::|::|  
 Db 16 TATCTCTCTCTTC 1

Search completed: June 19, 2007, 13:30:35  
 Job time : 611.5 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:49:12 ; Search time 6876 Seconds  
(without alignments)  
216.548 Million cell updates/sec

Title: US-10-604-726A-5136

Perfect score: 24  
Sequence: 1 uauugucucuccuucgccaccuc 24

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 35954

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*\*  
1: gb\_est1:\*\*  
2: gb\_est3:\*\*  
3: gb\_est4:\*\*  
4: gb\_est5:\*\*  
5: gb\_est6:\*\*  
6: gb\_est7:\*\*  
7: gb\_est8:\*\*  
8: gb\_est9:\*\*  
9: gb\_est10:\*\*  
10: gb\_est11:\*\*  
11: gb\_est12:\*\*  
12: gb\_est13:\*\*  
13: gb\_est14:\*\*  
14: gb\_est15:\*\*  
15: gb\_est16:\*\*  
16: gb\_est17:\*\*  
17: gb\_est18:\*\*  
18: gb\_est19:\*\*  
19: gb\_est20:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.4	55.8	25	15	AZ775852 2M0009N01
C 2	12.2	50.8	24	5	CA850924 D08B11 D2
C 3	12	50.0	23	15	AZ329650 1M0054A13
C 4	12	50.0	23	15	AZ514958 1M0054A13
C 5	11.6	48.3	21	15	AZ475883 1M0294J14
C 6	11.6	48.3	25	1	A1539240 tp64b08.x
C 7	11.2	46.7	18	9	CN750241 ApDT-VIII
C 8	11.2	46.7	21	19	AG189071 Pan trogl
C 9	11.2	46.7	21	19	AG202804 Pan trogl
C 10	11.2	46.7	22	10	CO788412 NT004AG0
C 11	11.2	46.7	25	17	CL692271 PRI0158C
C 12	11	45.8	19	17	CL671134 PRI0163D
C 13	11	45.8	22	1	AU014100
C 14	11	45.8	22	1	AU014106 AU014106

15 11 45.8 22 15 AZ942905  
16 11 45.8 23 19 CT014183  
17 10.8 45.0 25 1 A1527253  
18 10.8 45.0 25 15 AZ479489  
19 10.6 44.2 19 15 AZ345425  
20 10.6 44.2 23 19 TA376G03Q  
21 10.6 44.2 23 1 AJ797058  
22 10.6 44.2 23 13 DN759071  
23 10.6 44.2 23 15 AZ499076  
24 10.6 44.2 23 18 DX598444  
25 10.6 44.2 24 1 AJ792029  
26 10.6 44.2 24 19 AJ601047  
27 10.6 44.2 25 2 BG925523  
28 10.6 44.2 25 11 Z20702  
29 10.6 44.2 25 15 AZ333213  
30 10.6 44.2 25 15 AZ346715  
31 10.6 44.2 25 15 AZ490095  
32 10.4 43.3 21 8 CD533377  
33 10.4 43.3 21 8 CF318419  
34 10.4 43.3 21 13 DN955270  
35 10.4 43.3 22 1 AU014275  
36 10.4 43.3 23 15 AZ658085  
37 10.4 43.3 24 16 BH790181  
38 10.2 42.5 15 18 DX597598  
39 10.2 42.5 15 18 DX597599  
40 10.2 42.5 18 2 BG900971  
41 10.2 42.5 18 19 AJ587746  
42 10.2 42.5 19 15 AZ854740  
43 10.2 42.5 20 19 AG202286  
44 10.2 42.5 21 15 AZ342500  
45 10.2 42.5 22 1 A1057600

#### ALIGNMENTS

RESULT 1  
LOCUS AZ775852/c  
DEFINITION 2M0009N01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0009N01 F, genomic survey sequence.  
ACCESSION AZ775852  
VERSION AZ775852.1 GI:12902821  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, R., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0009 row: N column: 01  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers  
1. .25  
/organism="Mus musculus"

AZ942905 2M0203K13  
CT014183 KBRH122F2  
A1527253 uJ50E07.x  
AZ479489 1M0300H08  
AZ345425 1M0080A07  
AL497782 T. brucei  
AJ797058 AJ797058  
DN759071 G.hir-ste  
AZ499076 1M0336H08  
DX598444 Lewinski-  
AJ792029 AJ792029  
AJ601047 Arabidops  
BG925523 HNC5-1-D5  
Z20702 HSAACSBG V  
AZ333213 1M0062M11  
AZ346715 1M0082N06  
AZ490095 1M0322E15  
CD533377 31H19 Ara  
CF318419 HD--08-11  
DN955270 it84h07.9  
AU014275 AU014275  
AZ658085 1M0534J07  
BH790181 SALK 0565  
DX597598 Lewinski-  
DX597599 Lewinski-  
BG900971 HOA52-1-C  
AJ587746 Arabidops  
AZ854740 2M0158C01  
AG202286 Pan trogl  
AZ342500 1M0075A09  
A1057600 oy31d12.x



with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 50.0%; Score 12; DB 15; Length 23;  
Best Local Similarity 50.0%; Pred. No. 1.5e+06;  
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCC 12  
:|::|::|::|::|  
Db 11 TATTGTCCTCC 22

## RESULT 4

AZ514958 23 bp DNA linear GSS 05-OCT-2000  
LOCUS  
DEFINITION IM0054A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0054A13 F, genomic survey sequence.

ACCESSION AZ514958

VERSION AZ514958.1 GI:10696274

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A., and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0054 row: A column: 13

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

## FEATURES

## source

1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0054A13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 50.0%; Score 12; DB 15; Length 23;  
Best Local Similarity 50.0%; Pred. No. 1.5e+06;  
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAUGUCUCUCC 12  
:|::|::|::|::|  
Db 11 TATTGTCCTCC 22

## RESULT 5

AZ475883/c

## LOCUS

DEFINITION IM0294J14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0294J14 F, genomic survey sequence.

ACCESSION AZ475883

VERSION AZ475883.1 GI:10634008

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A., and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0294 row: J column: 14

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

## FEATURES

## source

1..21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0294J14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 48.3%; Score 11.6; DB 15; Length 21;  
Best Local Similarity 44.4%; Pred. No. 2.2e+06;  
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 7 CUCUCCUUGCCACCU 24

Db 21 CTCCTCTCTCCCTTC 4

## RESULT 6

AI539240/c  
LOCUS  
DEFINITION  
tp64b08.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2204055 3'  
similar to TR:Q40726 Q40726 DNA BINDING PROTEIN ; mRNA sequence.

ACCESSION  
AI539240

VERSION  
EST.

KEYWORDS  
Homo sapiens (human)

SOURCE  
Homo sapiens

ORGANISM  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 25)

AUTHORS  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 1192 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

## FEATURES

source

1..25 Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2204055"

/tissue\_type="poorly-differentiated endometrial

adenocarcinoma, 2 pooled tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Ut3"

/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.45 kb. Life Technologies catalog #:

11541-018"

## ORIGIN

Query Match 48.3%; Score 11.6; DB 1; Length 25;  
Best Local Similarity 44.4%; Pred. No. 2.3e+06;  
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 UCUCUCCUUGCCACCU 23

Db 25 TTCCCTTCCTCCCTCT 8

## RESULT 7

AI539240/c

LOCUS

DEFINITION

AI539240

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Acyrtosiphon pisum

(pea aphid)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 18)

AUTHORS

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.

An expressed sequence tags database for the pea aphid Acyrthosiphon

pisum

Unpublished (2004)

CONTACT: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory

(Buchnera) or facultative endosymbionts.

PCR Primers

FORWARD: GCCGCATCAACTCGTATAGCA

Plate: VIII row: C column: 12.

Location/Qualifiers

1..18

/organism="Acyrtosiphon pisum"

/mol\_type="mRNA"

/cultivar="intra-lyon-bf21 1101"

/db\_xref="taxon:7029"

/clone="ApDTVIIIC12"

/tissue\_type="digestive track"

/dev\_stage="adults, parthenogenetic females"

/lab\_host="ApDT"

/note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;

Sample name: ApDT; plant growth place: UMR INRA-INGA BP21

; Sowing date: 03/04/2003; Harvesting date: 12/06/2003;

Description: Long photoperiod 16-hr light/8-hr dark at 20

C; no overcrowding; grown on Vicia faba 3-wk old seedlings

sown under non sterile condition.; experimental

condition: standard, see description"

## ORIGIN

Query Match 46.7%; Score 11.2; DB 9; Length 18;

Best Local Similarity 31.2%; Pred. No. 3.3e+06;

Matches 5; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUUGUCUCCUUC 16

Db 16 TCTTTCTCTCTCTC 1

RESULT 8

AG189071/c

LOCUS

DEFINITION

AG189071

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AG189071

AG189071.1

GI:45221247

GSS.

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

18 bp mRNA linear EST 19-MAY-2004  
ApDT-VIII-C12 ApDT Acyrthosiphon pisum cDNA clone ApDTVIIIC12 5';  
mRNA sequence.

CN750241

CN750241

CN750241.1

GI:47515238

EST.

Acyrtosiphon pisum

(pea aphid)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 18)

AUTHORS

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.

An expressed sequence tags database for the pea aphid Acyrthosiphon

pisum

Unpublished (2004)

CONTACT: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory

(Buchnera) or facultative endosymbionts.

PCR Primers

FORWARD: GCCGCATCAACTCGTATAGCA

Plate: VIII row: C column: 12.

Location/Qualifiers

1..18

/organism="Acyrtosiphon pisum"

/mol\_type="mRNA"

/cultivar="intra-lyon-bf21 1101"

/db\_xref="taxon:7029"

/clone="ApDTVIIIC12"

/tissue\_type="digestive track"

/dev\_stage="adults, parthenogenetic females"

/lab\_host="ApDT"

/note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;

Sample name: ApDT; plant growth place: UMR INRA-INGA BP21

; Sowing date: 03/04/2003; Harvesting date: 12/06/2003;

Description: Long photoperiod 16-hr light/8-hr dark at 20

C; no overcrowding; grown on Vicia faba 3-wk old seedlings

sown under non sterile condition.; experimental

condition: standard, see description"



TAG\_LIB=NT"

## ORIGIN

Query Match 46.7%; Score 11.2; DB 10; Length 22;  
 Best Local Similarity 31.2%; Pred. No. 3.4e+06;  
 Matches 5; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUUGUCUCUCUUCG 17  
 |:::|:::|  
 Db 1 ATTATATCTACTTTCG 16

## RESULT 11

CL692271/c  
 LOCUS CL692271.1 GI:50214179 25 bp DNA linear GSS 10-JUL-2004  
 DEFINITION PR10158c\_P07\_2 - PR10158c.BR (25) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL692271  
 VERSION CL692271.1 GI:50214179  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; Pristionchus.

## REFERENCE

1 (bases 1 to 25)  
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
 AppADB: an AcedB database for the nematode satellite organism

## AUTHORS

## TITLE

Pristionchus pacificus

## JOURNAL

Nucleic Acids Res. 32. (1), D421-D422 (2004)

## PUBMED

## COMMENT

14681447  
 Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: fosmid ends.

FEATURES  
 source

1.25  
 Location/Qualifiers  
 /organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Mixed stage fosmid library of P. pacificus  
 var. California"  
 /note="Vector: pEpifos-5 Fosmid vector"

## ORIGIN

Query Match 46.7%; Score 11.2; DB 17; Length 25;  
 Best Local Similarity 37.5%; Pred. No. 3.4e+06;  
 Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAUGUCUCUCUUC 16  
 ::::|:::|  
 Db 17 TCTGCTCTCGCTTC 2

## RESULT 12

CL671134/c  
 LOCUS CL671134.1 GI:50169817 19 bp DNA linear GSS 09-JUL-2004  
 DEFINITION PR10163d.H11 - PR10163d.B21 (19) Note: Recurring String Mixed stage  
 fosmid library of P. pacificus var. California Pristionchus  
 pacificus genomic, genomic survey sequence.

ACCESSION CL671134  
 VERSION CL671134.1 GI:50169817  
 KEYWORDS GSS.  
 SOURCE Pristionchus pacificus  
 ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
 Neodiplogasteridae; Pristionchus.

1 (bases 1 to 19)  
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
 AppADB: an AcedB database for the nematode satellite organism  
 Pristionchus pacificus  
 Nucleic Acids Res. 32. (1), D421-D422 (2004)

## PUBMED

## COMMENT

14681447  
 Contact: Sommer RJ  
 Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: fosmid ends.

FEATURES  
 Location/Qualifiers

1.19  
 source

/organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Mixed stage fosmid library of P. pacificus  
 var. California"  
 /note="Vector: pEpifos-5 Fosmid vector"

## ORIGIN

Query Match 45.8%; Score 11; DB 17; Length 19;  
 Best Local Similarity 45.5%; Pred. No. 4e+06;  
 Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 5 GUCUCUCUUU 15  
 |:::|:::|  
 Db 15 GTCTCTCTCTTT 5

## RESULT 13

AU014100  
 LOCUS AU014100 Schizosaccharomyces pombe late log phase cDNA  
 DEFINITION Schizosaccharomyces pombe cDNA clone spc09165, mRNA sequence.

ACCESSION AU014100  
 VERSION AU014100.1 GI:3368891  
 KEYWORDS EST.  
 SOURCE Schizosaccharomyces pombe (fission yeast)  
 ORGANISM Schizosaccharomyces pombe  
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 Schizosaccharomycetales; Schizosaccharomycetaceae;  
 Schizosaccharomycetes.

## REFERENCE

## AUTHORS

## TITLE

Identification of expressed sequence tags of Schizosaccharomycetes

## JOURNAL

## COMMENT

Unpublished (1998)  
 Contact: Mitsuo Morimyo  
 Genome Research Group  
 National Institute of Radiological Sciences  
 9-1, Anagawa-4-chome, Inage-ku, Chiba 263-8555, Japan  
 Email: morimyo@nirs.go.jp.

FEATURES  
 source

1..22  
 Location/Qualifiers  
 /organism="Schizosaccharomyces pombe"  
 /mol\_type="mRNA"  
 /strain="972"  
 /db\_xref="taxon:4896"  
 /clone="spc09165"  
 /sex="h minus"  
 /clone\_lib="Schizosaccharomyces pombe late log phase cDNA"  
 /note="Vector: M13mp19; The cDNA library of  
 Schizosaccharomyces pombe was prepared by cloning cDNA"





Result No.	Query			ID	Description		
	Score	Match	Length				
C	1	21.4	25.2	50	2	AR683427	Sequence
	2	21.4	25.2	50	2	AR824195	Sequence
	3	20.8	24.5	76	2	B0437654	POLYNUCLE
	4	20.8	24.5	76	2	AX455957	Sequence
	5	20.8	24.5	76	10	AX047230S1	AX047230 HIV-1 TVO
C	6	20	23.5	60	2	B0469930	OLIGONUCL
	7	20	23.5	60	2	C0539417	Sequence
	8	19.8	23.3	83	2	AX982586	Sequence
	9	19.8	23.3	83	2	BD117445	EST and e
	10	19.8	23.3	83	2	AR421892	Sequence
	11	19.2	22.6	51	2	DD162947	Nucleic A
	12	19.2	22.6	60	5	AF011577	Homo sapi
	13	19.2	22.6	65	2	B0487569	OLIGONUCL
	14	19.2	22.6	65	2	C0557056	Sequence
	15	19	22.4	50	2	AR686075	Sequence
	16	19	22.4	50	2	AR826843	Sequence
	17	19	22.4	51	5	HSDTCRV03	Z37181 H. sapiens r
	18	18.8	22.1	50	2	C0005106	Sequence

```

ORIGIN
Query Match 25.2%; Score 21.4; DB 2; Length 50;
Best Local Similarity 41.0%; Pred. No. 1.3e+04;
Matches 16; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 42 AGUUGGAGGGCGCUUUGCUUGUUUUGGGAUGCAGA 80
      ||| ||| : : : : : ||| : : |
      ||| ||| : : : : : ||| : : |
Db 1 AGTCCCAAGGGTGTTTGTACTGTTTCTCCAATGAATA 39

RESULT 2
AR824195 LOCUS
DEFINITION Sequence 2856 from patent US 7026121.
ACCESSION AR824195
VERSION AR824195.1 GI:111848010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.

```

SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1
TITLE	zur Megede,J., Barnett,S.W., Engelbrecht,S. and van Rensburg,E. Polynucleotides encoding antigenic hiv type c polypeptides, polypeptides and uses thereof
JOURNAL	Patent: WO 0204493-A 73 17-JAN-2002; CHIRON CORPORATION (US); University of Stellenbosch (ZA)
FEATURES	Location/Qualifiers 1..76 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="HIV Type C RevExon1 Wild Type"
ORIGIN	
Query Match	24.5%; Score 20.8; DB 2; Length 76;
Best Local Similarity	41.1%; Pred. No. 2.2e+04;
Matches	23; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
QY	15 UGAGAGGGCGUGUUAAGCGGCCAAGUGAAGCGCGCUUUGCUCUGUUUUC 70 ::   ::: : : : :    :::   : : :   : : :   71 TGA TAGAGGATTTTGATGATCTTCACCACTTGGAGGAGCGCTTCGTGC GTCTCC 16
Db	
RESULT 5	
AY047230S1/c	
LOCUS	AY047230S1 76 bp DNA linear VRL 22-FEB-2002
DEFINITION	HIV-1 TV001 from South Africa Rev (rev) gene, exon 1.
ACCESSION	AY047230
VERSION	AY047230.1 GI:16554987
KEYWORDS	1 of 2
SEGMENT	Human immunodeficiency virus 1 (HIV-1)
SOURCE	Human immunodeficiency virus 1
ORGANISM	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group. 1 (bases 1 to 76) Scriba,T.J., de Villiers,T., Treurnicht,F.K., zur Megede,J., Barnett,S.W., Engelbrecht,S. and van Rensburg,E.J. Characterization of the South African HIV type 1 subtype C complete 5' long terminal repeat, nef, and regulatory genes AIDS Res. Hum. Retroviruses 18 (2), 149-159 (2002) 11839148 2 (bases 1 to 76) Scriba,T.J., de Villiers,T., Treurnicht,F.K., zur Megede,J., Barnett,S.J., Engelbrecht,S. and Janse van Rensburg,E. Direct Submission Submitted (04-JUL-2001) Department of Medical Virology, University of Stellenbosch, PO Box 19063, Tygerberg, Western Cape 7505, South Africa
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
PUBMED	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	Location/Qualifiers 1..76 /organism="Human immunodeficiency virus 1" /proviral /mol_type="genomic DNA" /isolate="TV001" /db_xref="taxon:11676" /country="South Africa" /note="Subtype: C" 1..76 /gene="rev" /number=1
source	
exon	
ORIGIN	
Query Match	24.5%; Score 20.8; DB 10; Length 76;
Best Local Similarity	41.1%; Pred. No. 2.2e+04;
Matches	23; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
QY	15 UGAGAGGGCGUGUUAAGCGGCCAAGUGAAGCGCGCUUUGCUCUGUUUUC 70 ::   ::: : : : :    :::   : : :   : : :   71 TGA TAGAGGATTTTGATGATCTTCACCACTTGGAGGAGCGCTTCGTGC GTCTCC 16
Db	

```

Component      inc: 08/
Location/Qualifiers
1. .60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match      23.5%; Score 20; DB 2; Length 60;
Best Local Similarity 38.9%; Pred. No. 4.5e+04;

```

RESULT	9
LOCUS	BD117445
LINEAR	83 bp DNA PAT 18-SEP-2002
DEFINITION	EST and encoded human protein.
ACCESSION	BD117445
VERSION	BD117445.1 GI:23212349
KEYWORDS	JP 2002010789-A/9522.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 83) Edwards,J.B.D.M., Jobert,S. and Giordano,J.E. EST and encoded human protein Patent: JP 2002010789-A 9522 15-JAN-2002; GENSET CORP
COMMENT	OS Homo sapiens (human) PN JP 2002010789-A/9522 PD 15-JAN-2002 PF 07-AUG-2000 JP 2000280989 PR 05-AUG-1999 US 60/147499 PI JEAN HAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT JEAN EVE PI GIORDANO PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC C12N1/21, PC C12N5/10,C12P21/02,C12P21/08,C13Q1/68,C12N15/00,C12N5/00, PC C12N15/00 CC EST and encoded human protein



```

/genes="BV655-BJ1SS"
/note="T cell receptor junctional region"

ORIGIN
Query Match      22.6%; Score 19.2; DB 5; Length 60;
Best Local Similarity 45.0%; Pred. No. 9.2e+04;
Matches 18; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 34 CGUCCCAAGUGAAGGCGCUUUGCUUCUGUUUUCUGG 73
    |||||:|||||:|||||:|||||:|||||:|||||:
Db 52 CATCACCAAAATGCTGGGCTGATTGCCACTGTTTCGGG 13

RESULT 13
BD487569
LOCUS      BD487569                65 bp    DNA    linear    PAT 04-NOV-2005
DEFINITION OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
VARIANTS THAT POPULATE A TRANSCRIPTOME.
ACCESSION  BD487569
VERSION    BD487569.1 GI:92356846
KEYWORDS  JP 2004508019-A/26691.
SOURCE    unidentified
ORGANISM  unclassified sequences.
REFERENCE  1 (bases 1 to 65)
AUTHORS   Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE     OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
VARIANTS THAT POPULATE A TRANSCRIPTOME
JOURNAL   Patent: JP 2004508019-A 26691 18-MAR-2004;
          Avi SHOSHAN,Alon WASSERMAN,Eli MINTZ,Liat MINTZ,Simchon FAIGLER
COMMENT   OS Mus musculus
          PN JP 2004508019-A/26691
          PD 18-MAR-2004
          PF 20-JUL-2001 JP 2002516365
          PR 02-MAY-2001 US 60/287724, 28-JUL-2000 US 60/221607 PI
          faigler
          CC

FH Key      Location/Qualifiers
FEATURES   source
           1..65
           /organism="unidentified"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32644"

ORIGIN
Query Match      22.6%; Score 19.2; DB 2; Length 65;
Best Local Similarity 41.7%; Pred. No. 9.2e+04;
Matches 20; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Qy 25 UGGUUAAGGCGUCCCAAGUGGAAGGCGCUUUGCUUCUGUUUUCUG 72
    :|||:|||||:|||||:|||||:|||||:|||||:
Db 12 TGCTGTAGTGATCCCTGGTGGAAAGCGGCCATGCTTCGTCTCG 59

RESULT 14
CO557056
LOCUS      CO557056                65 bp    DNA    linear    PAT 30-JAN-2004
DEFINITION Sequence 26691 from Patent WO0210449.
ACCESSION  CO557056
VERSION    CO557056.1 GI:41523483
KEYWORDS  Mus musculus (house mouse)
SOURCE    Mus musculus
ORGANISM  Mus musculus
REFERENCE  1
AUTHORS   Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE     Oligonucleotide library for detecting rna transcripts and splice
          variants that populate a transcriptome
JOURNAL   Patent: WO 0210449-A 26691 07-FEB-2002;
          Compugen Inc. (US)

FEATURES   source
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           /organism="unidentified"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32644"

ORIGIN
Query Match      22.4%; Score 19; DB 2; Length 50;
Best Local Similarity 41.9%; Pred. No. 1.1e+05;
Matches 18; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 38 CCCAAGUUGGAAGGCGCGCUUUGCUUCUGUUUUCUGAUGCAGA 80
    ||||:|||||:|||||:|||||:|||||:|||||:
Db 2 CCTCAGTACAAAGGCGGCTTTGGAAGTGTGTTGGCTGAATA 44

Search completed: June 19, 2007, 18:35:09
Job time : 10162 secs
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FEATURES   source
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           /mol_type="unassigned DNA"
           /db_xref="taxon:10090"

ORIGIN
Query Match      22.6%; Score 19.2; DB 2; Length 65;
Best Local Similarity 41.7%; Pred. No. 9.2e+04;
Matches 20; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Qy 25 UGGUUAAGGCGUCCCAAGUGGAAGGCGCUUUGCUUCUGUUUUCUG 72
    :|||:|||||:|||||:|||||:|||||:|||||:
Db 12 TGCTGTAGTGATCCCTGGTGGAAAGCGGCCATGCTTCGTCTCG 59

RESULT 15
AR686075
LOCUS      AR686075                50 bp    DNA    linear    PAT 12-SEP-2005
DEFINITION Sequence 5504 from patent US 6905827.
ACCESSION  AR686075
VERSION    AR686075.1 GI:74467845
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Wohlgemuth,J., Fry,K., Woodward,R. and Ly,N.
TITLE     Methods and compositions for diagnosing or monitoring auto immune
          and chronic inflammatory diseases
JOURNAL   Patent: US 6905827-A 5504 14-JUN-2005;
          Expression Diagnostics, Inc.; So. San Francisco, CA
FEATURES   source
           1..50
           /organism="unknown"
           /mol_type="genomic DNA"

ORIGIN
Query Match      22.4%; Score 19; DB 2; Length 50;
Best Local Similarity 41.9%; Pred. No. 1.1e+05;
Matches 18; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 38 CCCAAGUUGGAAGGCGCGCUUUGCUUCUGUUUUCUGAUGCAGA 80
    ||||:|||||:|||||:|||||:|||||:|||||:
Db 2 CCTCAGTACAAAGGCGGCTTTGGAAGTGTGTTGGCTGAATA 44

Search completed: June 19, 2007, 18:35:09
Job time : 10162 secs
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GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 15:35:52 ; Search time 314 Seconds  
(without alignments)  
2006.045 Million cell updates/sec

Title: US-10-604-726A-6033  
Perfect score: 85  
Sequence: 1 ggguaucgcaacagagag.....uuuucggaugcagaguccu 85

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 6044068

Minimum DB seq length: 0

Maximum DB seq length: 85

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_200701.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001as.\*
- 5: Geneseq2001bs.\*
- 6: Geneseq2002as.\*
- 7: Geneseq2002bs.\*
- 8: Geneseq2003as.\*
- 9: Geneseq2003bs.\*
- 10: Geneseq2003cs.\*
- 11: Geneseq2003ds.\*
- 12: Geneseq2004as.\*
- 13: Geneseq2004bs.\*
- 14: Geneseq2005s.\*
- 15: Geneseq2006s.\*
- 16: Geneseq2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.4	25.2	50	6 ABZ02865	Abz02865 Human leu
2	20.8	24.5	76	6 ABL33994	ABL33994 Wild type
3	20.8	24.5	76	12 ADM73807	Adm73807 HIV-1 pol
4	20	23.5	60	6 ABN36304	Abn36304 Human spl
5	19.6	23.1	51	10 ADK19849	Adk19849 Human man
6	19.6	23.1	74	10 ADK19487	Adk19487 Type IIs
7	19.2	22.6	60	15 ABK61465	Abk61465 Secreted
8	19.2	22.6	65	6 ABM53943	Abm53943 Mouse spl
9	19.2	22.6	80	12 ADM95921	Adm95921 Rat antis
10	19	22.4	50	6 ABZ05513	Abz05513 Human leu
11	19	22.4	60	14 AEC75978	Aec75978 Cancer pr
12	19	22.4	60	15 AEJ81361	Aej81361 Human cDN
13	18.8	22.1	50	4 AAL30539	Aal30539 Human SNP
14	18.8	22.1	50	4 AAL30538	Aal30538 Human SNP
15	18.8	22.1	60	2 AAX33875	Aax33875 HPV-16 in
16	18.8	22.1	65	6 ABN31277	Abn31277 Rat splic
17	18.8	22.1	70	14 ADZ27768	Adz27768 Chemosens

18	18.6	21.9	51	4 AAI75868	Aai75868 Human sil
19	18.6	21.9	60	6 ABN34367	Abn34367 Human spl
c 20	18.6	21.9	60	15 AEL67275	Ael67275 Murray re
c 21	18.6	21.9	60	15 AEL69636	Ael69636 Murray re
c 22	18.6	21.9	65	6 ABN27281	Abn27281 Rat splic
c 23	18.6	21.9	78	2 AAT21804	Aat21804 Human gen
c 24	18.4	21.6	43	2 AAQ85150	Aaq85150 Ureaplas
c 25	18.4	21.6	43	2 AAQ85118	Aaq85118 Ureaplas
c 26	18.4	21.6	43	2 AAQ85119	Aaq85119 Ureaplas
c 27	18.4	21.6	43	2 AAQ85138	Aaq85138 Ureaplas
28	18.4	21.6	50	15 AEG86030	Aeg86030 Hematolog
29	18.4	21.6	54	15 AEJ57607	Aej57607 SARS coro
30	18.4	21.6	54	15 AEK13577	Aek13577 SARS coro
31	18.4	21.6	69	2 AAT88275	Aat88275 M17 synth
32	18.4	21.6	70	14 ADY93938	Ady93938 Codon opt
c 33	18.4	21.6	70	14 ADY93993	Ady93993 Codon opt
c 34	18.4	21.6	85	6 ABL50273	AbL50273 Chimeric
c 35	18.2	21.4	40	13 ADU09560	Adu09560 Amidase p
c 36	18.2	21.4	40	15 AEF80899	Aef80899 Comamonas
c 37	18.2	21.4	40	15 AEF87849	Aef87849 C. testos
38	18.2	21.4	59	10 ACD95017	Acd95017 Human col
39	18.2	21.4	60	6 ABN32231	Abn32231 Human spl
c 40	18.2	21.4	60	14 AED19289	Aed19289 E. coli s
c 41	18.2	21.4	65	6 ABN58415	Abn58415 Mouse spl
c 42	18.2	21.4	65	6 ABN30268	Abn30268 Rat splic
c 43	18.2	21.4	65	15 AEI67892	Aei67892 DNA encod
44	18	21.2	37	11 ADO70341	Ado70341 PCR prime
c 45	18	21.2	40	6 ABN88696	Abn88696 E2F aptam

## ALIGNMENTS

### RESULT 1

ABZ02865  
ID ABZ02865 standard; DNA; 50 BP.

XX

AC ABZ02865;

XX

DT 09-JAN-2003 (first entry)

XX

DE Human leukocyte gene expression profiling probe SEQ ID NO 2856.

XX

T7; leukocyte; gene expression profiling; allograft rejection;

XX

KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;

XX

KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;

XX

OS Homo sapiens.

XX

WO200257414-A2.

XX

PD 25-JUL-2002.

XX

PF 22-OCT-2001; 2001WO-US047856.

XX

PR 20-OCT-2000; 2000US-0241994P.

XX

PA 08-JUN-2001; 2001US-0296764P.

XX

(BIOC-) BIOCARDIA INC.

XX

PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;

XX

PI Ly N, Woodward R, Quertermous T, Johnson F;

XX

WPI; 2002-636525/68.

XX

DR New system for leukocyte expression profiling, diagnosing a disease, or

XX

PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis

XX

PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX

PS Claim 1; Page 418; Opp; English.

XX

CC The invention relates to a system for detecting gene expression, which

CC comprises one or two isolated DNA molecules that detect expression of a  
 CC gene, where the gene corresponds to any of 8143 oligonucleotides  
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful  
 CC for leukocyte expression profiling. It is particularly useful for  
 CC diagnosing a disease, monitoring (rate of) progression of a disease,  
 CC predicting therapeutic outcome, determining prognosis for a patient,  
 CC predicting disease complications in an individual or monitoring response  
 CC to treatment in an individual. The diseases include cardiac allograft  
 CC rejection, kidney allograft rejection, liver allograft rejection,  
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection  
 XX  
 SQ Sequence 50 BP; 12 A; 10 C; 9 G; 19 T; 0 U; 0 Other;  
 Query Match 25.2%; Score 21.4; DB 6; Length 50;  
 Best Local Similarity 41.0%; Pred. No. 6.1e+02;  
 Matches 16; Conservative 12; Mismatches 11; Indels 0; Gaps 0;  
 QY 42 AGUUGAAGGCGCUCUGUCUGUUGUUGUUGAUGCAGA 80  
 DB 1 AGTCCCAAGGGTGTGTTGTTACTGTTTCTCCATGATA 39  
 RESULT 2  
 ABL39994/c  
 ID ABL39994 standard; DNA; 76 BP.  
 XX  
 AC ABL39994;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 15-MAY-2002 (first entry)  
 XX  
 DE Wild type 8\_5\_TV1\_C\_ZA exon 1 of Rev polynucleotide SEQ ID NO:73.  
 XX  
 KW Human immunodeficiency virus type C; antigenic HIV type C protein;  
 KW immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef;  
 KW immunostimulant; gene therapy; gene; ds.  
 XX  
 OS Human immunodeficiency virus; type C.  
 XX  
 FN WO20020493-A2.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 05-JUL-2001; 2001WO-US021241.  
 XX  
 PR 05-JUL-2000; 2000US-00610313.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PA (UYST-) UNIV STELLENBOSCH.  
 XX  
 PI Zur Megede J, Barnett SW, Engelbrecht S, Van Rensburg EJ;  
 XX  
 DR WPI; 2002-154920/20.  
 XX  
 PT New polynucleotides encoding antigenic HIV Type C polypeptides, useful in  
 PT applications including DNA immunization or generation of packaging cell  
 PT lines, particularly in gene therapy.  
 XX  
 PS Example 1; Fig 44; 233pp; English.  
 XX  
 CC The present invention describes expression cassettes comprising a  
 CC polynucleotide sequence encoding a polypeptide comprising any of the HIV  
 CC type C polypeptides. The expression cassettes comprise any of the HIV  
 CC type C sequences encoding gag, pol, vif, vpr, tat, rev, vpu, env or nef  
 CC (i). (i) have immunostimulant activity and can be used in gene therapy.  
 CC The HIV type C polynucleotides are useful in applications including DNA  
 CC immunisation, generation of packaging cell lines, and production of HIV  
 CC type C proteins. The polynucleotides are particularly useful in gene  
 CC therapy and DNA immunisation applications. ABL39942 to ABL40054 and  
 CC ABB06204 to ABB06215 represent sequences used in the exemplification of  
 CC the present invention. (Updated on 29-AUG-2003 to standardise OS field)

SQ Sequence 76 BP; 27 A; 18 C; 20 G; 11 T; 0 U; 0 Other;  
 Query Match 24.5%; Score 20.8; DB 6; Length 76;  
 Best Local Similarity 41.1%; Pred. No. 1.2e+03;  
 Matches 23; Conservative 11; Mismatches 22; Indels 0; Gaps 0;  
 QY 15 UGAGAGGCGUGUUAAGGCGUCCCAAGUUGAAGGCGGCUUUGCUUGUUUC 70  
 DB 71 TGATAGAGGATTTTGATGATCTTCACCACTTGAGGAGCGCTTCGTCGTCTCC 16  
 RESULT 3  
 ADM73807/c  
 ID ADM73807 standard; DNA; 76 BP.  
 XX  
 AC ADM73807;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE HIV-1 polynucleotide #42.  
 XX  
 KW HIV-1; gene; ds; HIV pol; immune response; DNA immunisation;  
 KW HIV type C protein; immunostimulant.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 FN US2003223961-A1.  
 XX  
 PD 04-DEC-2003.  
 XX  
 PF 05-JUL-2001; 2001US-00899575.  
 XX  
 PR 05-JUL-2000; 2000US-00610313.  
 XX  
 PA (MECE/) MECEDE J Z.  
 PA (BARN/) BARNETT S W.  
 PA (ENGE/) ENGELBRECHT S.  
 PA (RENS/) RENSBURG E J V.  
 XX  
 PI Megede JZ, Barnett SW, Engelbrecht S, Rensburg EJV;  
 XX  
 DR WPI; 2004-060515/06.  
 XX  
 PT New expression cassette comprising a polynucleotide sequence encoding an  
 PT HIV Pol polypeptide, useful in eliciting an immune response, in DNA  
 PT immunization, generating of packaging cell lines or in producing HIV Type  
 PT C proteins.  
 XX  
 PS Example 1; SEQ ID NO 73; 160pp; English.  
 XX  
 CC The invention relates to an expression cassette comprising a  
 CC polynucleotide sequence encoding an HIV Pol polypeptide. The invention  
 CC also relates to a recombinant expression system for use in a host cell  
 CC comprising an expression cassette, where the polynucleotide sequence  
 CC further comprises control elements capable of driving expression in the  
 CC selected host cell, a cell comprising an expression cassette where the  
 CC polynucleotide sequence further comprises control elements compatible  
 CC with the expression in the cell and a composition for generating an  
 CC immunological response, comprising an expression cassette. The expression  
 CC cassette and the methods of the invention are useful in eliciting an  
 CC immune response, in DNA immunisation, in generation of packaging cell  
 CC lines and in producing HIV Type C proteins. This sequence represents an  
 CC HIV-1 polynucleotide of the invention.  
 XX  
 SQ Sequence 76 BP; 27 A; 18 C; 20 G; 11 T; 0 U; 0 Other;  
 Query Match 24.5%; Score 20.8; DB 12; Length 76;  
 Best Local Similarity 41.1%; Pred. No. 1.2e+03;  
 Matches 23; Conservative 11; Mismatches 22; Indels 0; Gaps 0;  
 QY 15 UGAGAGGCGUGUUAAGGCGUCCCAAGUUGAAGGCGGCUUUGCUUGUUUC 70  
 DB 71 TGATAGAGGATTTTGATGATCTTCACCACTTGAGGAGCGCTTCGTCGTCTCC 16



**Qy** 43 GUUGGAAGGCGCUUUCUGUUUUCUGGAUGCA 78  
||:||||| |:::||: |: :||  
**D6** 25 GTTGGGAAGACGGAATTGCTTTGGTAATCTGCTTC 60

ADK19487;  
06-MAY-2004 (first entry)  
Type IIS restriction enzyme construct #10.  
recognition site; type IIS restriction enzyme; nucleic acid library;  
ligation; ss.  
Unidentified.  
EP1314783-A1.  
28-MAY-2003.  
22-NOV-2001; 2001EP-00127864.  
22-NOV-2001; 2001EP-00127864.  
(SLON-) SLONING BIOTECHNOLOGY GMBH.  
Schatz O, O'Connell T;  
WPI; 2003-451033/43.  
New single-stranded nucleic acid, useful in parallel production of  
synthetic genes, includes a sequence containing type IIS enzyme  
recognition site and a defined sequence.  
Disclosure; Fig 7; 69pp; German.  
This invention describes the novel use of a single-stranded nucleic acid,  
for use in preparation of nucleic acid comprising a part (A) comprising  
the sequence of a recognition site for a type IIS restriction enzyme, or  
its fragments or complement, and a part (B) that is a defined sequence of  
nucleotides. The method of comprises preparing an oligonucleotide (ON1),  
optionally by modification of an oligonucleotide linked to a surface,  
that contains the recognition site (or fragment or complement) of a type  
IIS enzyme that cuts outside its recognition sequence to generate a  
single-stranded overhang. ON1 is ligated with the single-stranded nucleic  
acid, particularly where part (A) is complementary to the overhang, to  
form a 5'-overhang, which is filled in. A second oligonucleotide (ON2),  
similar to ON1 but with the recognition site for a different type IIS  
enzyme, is treated similarly and the two filled-in ligation products are  
ligated, then the product cleaved with one of the relevant enzymes.  
Particularly ON1 is on a solid phase but is released before ligation to  
the ON2-derived product. A second method involves preparing two partially  
double-stranded oligonucleotides (ON10, ON11) with a 3'-overhang and  
restriction sites for different type IIS enzymes and two groups of single  
-stranded nucleic acid consisting of part (A) complementary to the single  
-stranded region of ON10 or ON11, especially the same for all members of  
a group, and a 2 or 3-nt (B) that is different for each member of the  
group. ON10 and ON11 are hybridised then ligated to the appropriate  
groups of single-stranded nucleic acid, their 5'-ends filled in and the  
product from one group ligated with those of the other group. The  
products of this step are then cleaved with the type IIS enzyme that is  
specific for ON10, especially Sapi. ON10 and ON11 are reacted with each  
member of their groups, in individual reaction vessels, and they may be  
modified for coupling to a matrix. The enzyme recognition site is present  
partly in the overhang or entirely in the double-stranded region of ON10  
and ON11. Another method comprises ligating two partially double-stranded  
oligonucleotides (ON20, ON21) with 5'-overhangs of 3 nt which include a  
recognition site for type IIS enzyme, with ON20 modified so that it can  
be fixed to a solid matrix. Residual reactants and enzymes are removed,  
the product cleaved with the enzyme appropriate for ON21 and the  
resulting extended oligonucleotide (ONE) is separated and optionally the  
procedure repeated sequentially with additional oligonucleotides of the  
ON21 type. The same process is used to produce another ONE and the two  
final ONE are ligated in an orientation determined by blockade of the  
ends that are not intended for ligation. The product of this step is then  
cleaved with an type IIS enzyme that cuts in either of the ONE. The  
enzyme used creates a 3 nt overhang, except in the last repetition of the  
process leading to ONE, where it creates an overhang of other than 3 nt.

CC The nucleic acids are used to prepare nucleic acids, particularly  
CC synthetic genes, or nucleic acid libraries, particularly by sequential  
CC ligation of oligonucleotides in parallel reactors, in sequence-  
CC independent manner. The products of the invention makes possible sequence  
CC -independent linkage of different partial sequences, based on  
CC standardised components, i.e. an oligonucleotide library of relatively  
CC low complexity. This reduces the effort involved in producing a complete  
CC library of sequences, without problems of low ligation efficiency  
CC associated with 1 or 2 nucleotide overhangs, and the use of short  
CC oligonucleotides improves both yield and purity. The proportion of broken  
CC and failed sequences is reduced and many gene variants can be prepared  
CC simultaneously. This sequence represents a polynucleotide used to make  
CC the type IIS restriction enzyme constructs used to illustrate the method  
CC of the invention.

SQ Sequence 74 BP; 10 A; 22 C; 21 G; 21 T; 0 U; 0 Other;

Query Match 23.1%; Score 19.6; DB 10; Length 74;

Best Local Similarity 48.0%; Pred. No. 3.3e+03; Mismatches 19; Indels 0; Gaps 0;  
Matches 24; Conservative 7;

QY 15 UGAGAGGGGCGUGUUAAGCGGCCAAGUUGGAAGGGCGCUUUGCUUCU 64  
DB 13 TGAGAGCGCTTTTCGGCGCTCACCAGTCTGTAGAGCGCGCGGTTT 62

# RESULT 7

ASK61465

ID ASK61465 standard; DNA; 60 BP.

XX AC ASK61465;

XX DT 30-NOV-2006 (first entry)

XX DE Secreted soluble agrin variant PCR primer SEQ ID NO 8.

XX KW protein engineering; muscular-gen.; nootropic; neuroleptic;  
XX KW neuroprotective; enzyme inhibition; screening; atrophy; schizophrenia;  
XX KW cognitive disorder; head injury; cerebroprotective; vulnerary;  
XX KW neurological disease; cerebrovascular ischemia; vasotropic;  
XX KW multiple sclerosis; parkinsons disease; antiparkinsonian;  
XX KW Alzheimers disease; agrin; PCR; primer; ss.

XX OS Synthetic.

XX OS Unidentified.

XX PN WO2006103261-A2.

XX PD 05-OCT-2006.

XX PF 29-MAR-2006; 2006WO-EP061152.

XX PR 30-MAR-2005; 2005EP-00102481.

XX PA (UY2U-) UNIV ZUERICH.

XX PI Sonderegger P, Hettwer S, Bolliger MF, Dreier B, Kunz B;

XX PI Luescher D, Reif R, Sales S;

XX DR WPI; 2006-670399/69.

XX PT Determining neurotrophin inhibitor compound involves incubating compound  
XX with neurotrophin having protease domain, and agrin peptide comprising  
XX specified cleavage site; in aqueous buffer, and measuring amount of  
XX cleavage of agrin.

XX PS Example 20; SEQ ID NO 8; 91pp; English.

XX CC The invention describes a method of determining a neurotrophin inhibitor  
XX compound involves: (a) incubating the compound with neurotrophin, its  
XX variant or fragment comprising the protease domain of neurotrophin, and a  
XX protein or peptide comprising agrin, its variant or fragment comprising a  
XX cleavage site between arginine 995 and alanine 996, or lysine 1754 and

serine 1755; in an aqueous buffer solution; and measuring the amount of cleavage of agrin. Also described are: a method (M1) for measuring catalytic activity of neurotrophin involving: incubating neurotrophin, its variant or fragment comprising the protease domain with a protein or peptide comprising agrin, its variant or fragment comprising the cleavage site of agrin, in an aqueous buffer solution; and measuring the amount of cleavage of agrin; and neurotrophin inhibitor compounds of formula (I) and its addition salts. The method is useful for: determining a neurotrophin inhibitor compound; in a medicament for treatment and/or prophylaxis of diseases caused by deficiency of synapses, skeletal muscle atrophy, schizophrenia and cognitive disturbance; for measuring catalytic activity of neurotrophin; and for impairment of cognitive functions in patients with Alzheimer's disease, Parkinson's disease, multiple sclerosis, stroke, and head trauma. This sequence represents a primer used in the creation of an engineered secreted soluble agrin variant.

Sequence 60 BP; 8 A; 16 C; 19 G; 17 T; 0 U; 0 Other;

Query Match 22.6%; Score 19.2; DB 15; Length 60;  
Best Local Similarity 41.1%; Pred. No. 4.4e+03;  
Matches 23; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

OY 26 GGUUAAGGCGUCCCAAGUGGAGGCGCUUUCUUCUGUUCUGAUGCAGACAG 81  
DB 1 GCCTGCGCGCTCATTTTCGAACTCGGGTGGCTCCAGTTATCTAGATCCGGTG 56

## RESULT 9

ADM95921/c  
ID ADM95921 standard; DNA; 65 BP.

XX AC ADM95921;  
XX 15-JUL-2002 (first entry)

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:26691.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.

XX Mus musculus.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB001903.

XX 28-JUL-2000; 2000US-0221607P.

XX 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes.

XX Example 1; SEQ ID NO 26691; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or

quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue - and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 65 BP; 12 A; 15 C; 19 G; 19 T; 0 U; 0 Other;

Query Match 22.6%; Score 19.2; DB 6; Length 65;  
Best Local Similarity 41.7%; Pred. No. 4.5e+03;  
Matches 20; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

OY 25 UGUUAAGGCGUCCCAAGUGGAGGCGCUUUCUUCUGUUCUUCUG 72

DB 12 TGCTGTAGTGATCCCTGCTGGAAGGCGGCATGCTTCTGCTCTG 59

## RESULT 9

ADM95921/c  
ID ADM95921 standard; DNA; 80 BP.

XX AC ADM95921;  
XX 01-JUL-2004 (first entry)

DE Rat antisense oligonucleotide #814.

XX Rat; antisense oligonucleotide; ss; antisense RNA production; oncogenes;  
KW tumour suppressor; cell cycle regulator; ion channel protein;  
KW transport protein; intracellular signal transduction;  
KW transcription factor; DNA-binding protein;  
KW cell-cell communication protein; stress response gene;  
KW apoptosis related gene; growth factor; chemokine; interleukin;  
KW interferon; hormone; neurotransmitter; cell surface antigen;  
KW cell adhesion molecule.

XX Rattus sp.

XX US2004072191-A1.

XX 15-APR-2004.

XX 07-MAR-2003; 2003US-00384245.

XX 07-MAR-2002; 2002US-0362823P.

XX (CHEN/) CHENCHIK A.

XX Chenchik A;

XX WPI; 2004-373913/35.

XX New standardizing control for RNA samples to be tested on non-control gene sequences on nucleic acid arrays, useful for producing a population of distinct antisense RNA molecules from an initial population of distinct mRNA molecules.

XX Disclosure; SEQ ID NO 814; 282pp; English.

XX The invention relates to a standardising control for RNA samples to be tested on non-control gene sequences on nucleic acid arrays, comprising a pool of unique tagged synthetic antisense mRNA molecules of a known concentration, where any two sequences are unique if their sequences differ. The non-control gene sequences on the nucleic acid array comprise



CC such as breast cancer, diabetes, autoimmune, neurodegenerative disorder  
CC and obesity. The method provides improved prognostic process to provide  
CC appropriate course of prophylaxis and therapy. This sequence represents a  
CC genetic marker associated with cancer prognosis.

XX SQ Sequence 60 BP; 13 A; 16 C; 15 G; 16 T; 0 U; 0 Other;

Query Match 22.4%; Score 19; DB 14; Length 60;  
Best Local Similarity 51.2%; Pred. No. 5.2e+03;  
Matches 22; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 GGGUUAUCUGCAACUGAGAGGGGCGUGUUAAGGCGUCCCAAG 43  
|| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 55 GGTATTTCATCTTCAGGGGTGGAAGAGCTGTCCCAAG 13

## RESULT 12

AEJ81361/c  
ID AEJ81361 standard; cDNA; 60 BP.

XX AC AEJ81361;

XX DT 19-OCT-2006 (first entry)

XX DE Human cDNA diagnostic/prognostic for breast cancer NM\_004207 #2.

XX KW Diagnosis; prognosis; ss; breast tumor; cancer; cytostatic; neoplasm;  
XX KW DNA microarray; gene expression; tumor marker.

XX OS Homo sapiens.

XX PN WO2006084272-A2.

XX PD 10-AUG-2006.

XX PF 06-FEB-2006; 2006WO-US004280.

XX PR 04-FEB-2005; 2005US-0650365P.

XX PA (ROSE-) ROSETTA INPHARMATICS LLC.

XX PA (MERI ) MERCK & CO INC.

XX PI Dai H, Friend SH, Deutsch P;

XX DR WPI; 2006-613101/63.

XX PT Predicting responsiveness of breast cancer patient to chemotherapy based  
XX on patient's cellular constituent profile, comprises measurement of  
XX cellular constituents, estrogen receptor (ER) level and ER level relative  
XX to patient's age.

XX PS Disclosure; SEQ ID NO 140; 349pp; English.

XX CC The invention relates to predicting responsiveness of a breast cancer  
XX patient to chemotherapy, comprising predicting the patient to exhibit  
XX enhanced response to chemotherapy as compared to patients in the general  
XX population of breast cancer patients if the cellular constituent profile  
XX is a poor prognosis profile, and the estrogen receptor (ER) level is ER+  
XX, and the ER level relative to patient's age (ER/AGE) is low. Also  
XX included are selecting a patient for enrollment in a clinical trial of a  
XX drug for treating breast cancer (based on the cellular constituent  
XX profile, ER level and an ER/AGE), identifying a breast cancer patient as  
XX a good or poor candidate for chemotherapy (based on the cellular  
XX constituent profile, ER level and an ER/AGE) and a computer system and  
XX program for carrying out the predicting, selecting and identifying  
XX methods. In the predicting method, the ER level is determined by  
XX measuring an expression level of a gene encoding the ER in the patient  
XX relative to expression level of the gene in the control sample. The gene  
XX encoding the ER is the ERalpha gene. The estrogen receptor level is  
XX measured by an oligonucleotide probe. The chemotherapy is carried out  
XX using cyclophosphamide, methotrexate and 5-fluorouracil. The method is  
XX useful for predicting responsiveness of a breast cancer patient to  
XX chemotherapy based on measurement of cellular constituents, ER level and

CC ER/AGE. The cellular constituent profile is used to determine patients  
CC suitable for clinical trials of a drug for treating breast cancer and  
CC determining if the patient is a good or poor candidate for chemotherapy.  
CC The method enables improved and high sensitive prediction of the  
CC responsiveness of a breast cancer patient to chemotherapy. The present  
CC sequence is a fragment of a human cDNA whose differential expression  
CC level makes it a candidate for the cellular constituent profile.

XX SQ Sequence 60 BP; 13 A; 16 C; 15 G; 16 T; 0 U; 0 Other;  
Query Match 22.4%; Score 19; DB 15; Length 60;  
Best Local Similarity 51.2%; Pred. No. 5.2e+03;  
Matches 22; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 GGGUUAUCUGCAACUGAGAGGGGCGUGUUAAGGCGUCCCAAG 43  
|| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
Db 55 GGTATTTCATCTTCAGGGGTGGAAGAGCTGTCCCAAG 13

## RESULT 13

AAL30539

ID AAL30539 standard; DNA; 50 BP.

XX AC AAL30539;

XX DT 24-JAN-2002 (first entry)

XX DE Human SNP oligonucleotide #3747.

XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
XX KW neuroprotective; antimicrobial; gene therapy; vaccine; cancer;  
XX KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
XX KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
XX KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
XX KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
XX KW multifactorial disease; autoimmune disease; infection;  
XX KW nervous system disease; ss.

XX OS Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US035498.

XX PR 28-DEC-1999; 99US-0173419P.

XX PR 27-DEC-2000; 2000US-00173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX DR WPI; 2001-465210/50.

XX CC Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
XX autoimmune diseases and infections.

XX Claim 1; Page 2462; 4143pp; English.

XX CC The present invention relates to oligonucleotides encoding polymorphic  
XX variants of proteins related to amylases, amyloid proteins, angiotensin,  
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
XX histones, kinases, colony stimulating factors, complement related  
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
XX protein coupled receptors and thioesterases. The present sequence is one  
XX such oligonucleotide. The oligonucleotides and the peptides encoded by  
XX them may be used in the prevention, diagnosis and treatment of diseases  
XX associated with inappropriate expression of the proteins listed above.  
XX Disorders that may be prevented, diagnosed and/or treated include  
XX multifactorial diseases with a genetic component, such as autoimmune  
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,

CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms  
SQ Sequence 50 BP; 12 A; 9 C; 21 G; 8 T; 0 U; 0 Other;  
XX

Query Match 22.1%; Score 18.8; DB 4; Length 50;  
Best Local Similarity 56.5%; Pred. No. 5.9e+03;  
Matches 26; Conservative 3; Mismatches 17; Indels 0; Gaps 0;  
QY 9 UGCAACUGAGAGGGGCGUGUUAAGGCGUCCCAAGUUGGAAGGGCG 54  
DB 4 TGCACCTTACGGGGCTGGAGAGGCGCTGGATAAAGACAGAGGGCG 49

RESULT 14  
AAL30538  
ID AAL30538 standard; DNA; 50 BP.  
XX  
AC AAL30538;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #3746.  
XX

Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
neuroprotective; antimicrobial; gene therapy; vaccine; cancer;  
myeloid protein; angiopoietin; apoptosis related protein; cadherin;  
cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
complement related protein; cytochrome; kinesin; cytokine; interferon;  
interleukin; G-protein coupled receptor; thioesterase; inflammation;  
multifactorial disease; autoimmune disease; infection;  
nervous system disease; ss.

Homo sapiens.  
WO200147944-A2.  
05-JUL-2001.  
28-DEC-2000; 2000WO-US035498.  
28-DEC-1999; 99US-0173419P.  
27-DEC-2000; 2000US-00173419.  
(CURA-) CURAGEN CORP.  
Shinkets RA, Leach M;  
WPI; 2001-465210/50.  
Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
autoimmune diseases and infections.

Claim 1; Page 2462; 4143pp; English.  
The present invention relates to oligonucleotides encoding polymorphic  
variants of proteins related to amylases, amyloid proteins, angiopoietin,  
apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
histones, kinases, colony stimulating factors, complement related  
proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
protein coupled receptors and thioesterases. The present sequence is one  
such oligonucleotide. The oligonucleotides and the peptides encoded by  
them may be used in the prevention, diagnosis and treatment of diseases  
associated with inappropriate expression of the proteins listed above.  
Disorders that may be prevented, diagnosed and/or treated include  
multifactorial diseases with a genetic component, such as autoimmune  
diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
systemic lupus erythromatosus and Grave's disease), inflammation, cancer  
(e.g. cancers of the bladder, brain, breast, colon and kidney,  
leukaemia), diseases of the nervous system and an infection of pathogenic

CC organisms  
XX  
SQ Sequence 50 BP; 12 A; 10 C; 20 G; 8 T; 0 U; 0 Other;  
XX

Query Match 22.1%; Score 18.8; DB 4; Length 50;  
Best Local Similarity 56.5%; Pred. No. 5.9e+03;  
Matches 26; Conservative 3; Mismatches 17; Indels 0; Gaps 0;  
QY 9 UGCAACUGAGAGGGGCGUGUUAAGGCGUCCCAAGUUGGAAGGGCG 54  
DB 5 TGCACCTTACGGGGCTGGAGAGGCGCTGGATAAAGACAGAGGGCG 50

RESULT 15  
AAX33875/c  
ID AAX33875 standard; RNA; 60 BP.  
XX  
AC AAX33875;  
XX  
DT 25-JUN-1999 (first entry)  
XX  
DE HPV-16 inhibitor.  
XX  
KW HPV-16; inhibitor; antisense oligonucleotide; E6/E7 gene; human;  
KW keratinocyte; cervical cell; cervical tumour; ss.  
XX  
OS Synthetic.  
OS Human papillomavirus type 16.  
XX  
PN WO9913071-A1.  
XX  
PD 18-MAR-1999.  
XX  
PF 03-SEP-1998; 98WO-US018320.  
XX  
PR 05-SEP-1997; 97US-00929140.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Dipaolo J, Alvarez-Salas L;  
XX  
DR WPI; 1999-243727/20.  
XX  
PT New antisense oligonucleotide analogs for inhibiting growth of cervical  
tumors.

Disclosure; Page 7; 40pp; English.  
This sequence represents an antisense oligonucleotide of the invention.  
The antisense oligonucleotide analogs (ONs) have a sequence complementary  
to a sequence of nucleotides 415-445 of human papilloma virus-16 (HPV-  
16). The antisense ONs can be used to inhibit expression of HPV gene  
E6/E7 in living cells, preferably human keratinocytes or human cervical  
cells. They bind to E6/E7 mRNA in the cell, prevent mRNA translation and  
promote mRNA degradation by intracellular RNase H. They can be used for  
preventing transformation of living cells by HPV. The antisense ONs are  
used particularly for inhibiting the growth of cervical tumours

Sequence 60 BP; 14 A; 15 C; 15 G; 0 T; 16 U; 0 Other;  
XX  
Query Match 22.1%; Score 18.8; DB 2; Length 60;  
Best Local Similarity 41.3%; Pred. No. 6.2e+03;  
Matches 19; Conservative 10; Mismatches 17; Indels 0; Gaps 0;  
QY 29 UAAGGCGUCCCAAGUUGGAAGGGCGGUUUGUUGUUCUUGUUGGA 74  
DB 49 TACCACGGACCGAAGTCCGTCGACGCTCTGTGACTGTCTCTGAA 4

Search completed: June 19, 2007, 16:30:34  
Job time : 317 secs

Result No.	Query			DB	ID	Description
	Score	Match	\$			
1	21.4	25.2	50	3	US-10-131-827-2856	Sequence 2856, Ap
2	21.4	25.2	50	5	US-10-131-831-2856	Sequence 2856, Ap
3	19.8	23.3	83	3	US-09-621-976-13389	Sequence 13389, A
4	19	22.4	50	3	US-10-131-827-15504	Sequence 5504, Ap
5	19	22.4	50	5	US-10-131-831-5504	Sequence 5504, Ap
C 6	18.8	22.1	61	3	US-08-929-140-9	Sequence 9, Appli
C 7	18.8	22.1	61	3	US-09-560-579A-9	Sequence 9, Appli
C 8	18.6	21.9	68	2	US-08-981-663-59	Sequence 59, Appl
C 9	18.6	21.9	76	2	US-08-981-663-61	Sequence 61, Appl
10	18.6	21.9	76	2	US-08-981-663-62	Sequence 62, Appl
C 11	18.6	21.9	76	2	US-08-981-663-65	Sequence 65, Appl
12	18.6	21.9	76	2	US-08-981-663-66	Sequence 66, Appl
13	18.4	21.6	43	3	US-08-109-037-22	Sequence 22, Appl
14	18.4	21.6	43	3	US-08-109-037-55	Sequence 55, Appl
C 15	18.4	21.6	43	3	US-08-109-037-56	Sequence 56, Appl
C 16	18.4	21.6	43	3	US-08-109-037-57	Sequence 57, Appl
17	18.4	21.6	69	3	US-09-025-769B-336	Sequence 336, App
18	18.4	21.6	69	3	US-09-490-070A-336	Sequence 336, App
19	18.4	21.6	69	3	US-09-490-153-336	Sequence 336, App
20	18.4	21.6	69	3	US-09-490-324-336	Sequence 336, App
21	17.8	20.9	50	3	US-10-131-827-2558	Sequence 2558, Ap
22	17.8	20.9	50	3	US-10-131-827-6041	Sequence 6041, Ap
23	17.8	20.9	50	3	US-10-131-827-6334	Sequence 6334, Ap

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; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5504
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-5504

Query Match      22.4%; Score 19; DB 3; Length 50;
Best Local Similarity 41.9%; Pred. No. 1e+03;
Matches 18; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY   38   CCCAAGTUGGAAGGCGCUUUGCUUCGUUUUUCUGGAUGCAGA 80
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db    2   CCTCAGTACAAAGGGCGCTTTGGAAGTGTTGTGGCTGAATA 44

RESULT 5
US-10-131-831-5504
; Sequence 5504, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Worlgenmuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131.831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5504
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-5504

Query Match      22.4%; Score 19; DB 5; Length 50;
Best Local Similarity 41.9%; Pred. No. 1e+03;
Matches 18; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY   38   CCCAAGTUGGAAGGCGCUUUGCUUCGUUUUUCUGGAUGCAGA 80
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db    2   CCTCAGTACAAAGGGCGCTTTGGAAGTGTTGTGGCTGAATA 44

RESULT 6
US-08-929-140-9/c
; Sequence 9, Application US/08929140
; Patent No. 6084090
; GENERAL INFORMATION:
; APPLICANT: DiPaolo, Joseph
; APPLICANT: Alvarez-Salas, Luis
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS INHIBITION
; TITLE OF INVENTION: BY ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive Sixteenth Flo
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 61 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-560-579A-9

Query Match          22.1%; Score 18.8; DB 3; Length 61;
Best Local Similarity 41.3%; Pred. No. 1.3e+03;
Matches 19; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY      29 URAAGCGUCUCCCCAAGUGAAGGCGCUUUGCUUGUUUUUCUGGA 74
       :| | | | | | | | | | | | | | | | | | | | | |
Db      49 TACCACGGACCGAAGTCCGTGTGACGCTGTGGTACTGTTCTCTGAA 4

RESULT 8
US-08-981-663-59/c
; Sequence 59, Application US/08981663
; Patent No. 5952176
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, THOMAS VALENTINE
; APPLICANT: VAUGHAN, PATRICK MARTIN
; TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AT CANDIDATE LOCI
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESS: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,663
FILING DATE: 08-JAN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1377-120P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
US-08-981-663-59

Query Match      21.9%; Score 18.6; DB 2; Length 68;
Best Local Similarity 51.2%; Pred. No. 1.6e+03;
Matches 21; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Oy 21 GGGCGUGUUAAGCGGUCGCCAAGUUGGAAGGGCGCUUUGCU 61
Db 43 GGGCGTGTGTTGGCCGGCCACTACGTGTTAGGTAGGTAGGT 3

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RESULT 9  
US-08-981-663-61/c  
; Sequence 61, Application US/08981663  
; Patent No. 5952176  
; GENERAL INFORMATION:  
; APPLICANT: MCCARTHY, THOMAS VALENTINE  
; APPLICANT: VAUGHAN, PATRICK MARTIN  
; TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AT CANDIDATE LOCI  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981.663  
; FILING DATE: 08-JAN-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SVENSSON, LEONARD R.  
; REGISTRATION NUMBER: 30,330  
; REFERENCE/DOCKET NUMBER: 1377-120P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 76 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 22  
; OTHER INFORMATION: /mod\_base= i  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 25  
; OTHER INFORMATION: /mod\_base= i  
; US-08-981-663-61

Query Match 21.9%; Score 18.6; DB 2; Length 76;  
Best Local Similarity 51.2%; Pred. No. 1.7e+03;  
Matches 21; Conservative 6; Mismatches 14; Indels 0; Gaps 0;  
Qy 21 GGGCUGGUUAAGCGGCCCAAGUUGGAGGCGCGCUUUGCU 61  
Db 43 GGGCTGGTTTGGCCGCCACTACGTGGTAGGTCAGGATGCT 3

RESULT 10  
US-08-981-663-62  
; Sequence 62, Application US/08981663  
; Patent No. 5952176  
; GENERAL INFORMATION:  
; APPLICANT: MCCARTHY, THOMAS VALENTINE  
; APPLICANT: VAUGHAN, PATRICK MARTIN  
; TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AT CANDIDATE LOCI  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia

COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/981.663  
FILING DATE: 08-JAN-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SVENSSON, LEONARD R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 1377-120P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 76 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 12  
OTHER INFORMATION: /mod\_base= i  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 22  
OTHER INFORMATION: /mod\_base= i  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 25  
OTHER INFORMATION: /mod\_base= i  
US-08-981-663-62

Query Match 21.9%; Score 18.6; DB 2; Length 76;  
Best Local Similarity 58.5%; Pred. No. 1.7e+03;  
Matches 24; Conservative 3; Mismatches 14; Indels 0; Gaps 0;  
Qy 21 GGGCUGGUUAAGCGGCCCAAGUUGGAGGCGCGCUUUGCU 61  
Db 34 GGGCTGGTTTGGCCGCCACUACUGGUGAGGUCAGGAGCU 74

RESULT 11  
US-08-981-663-65/c  
; Sequence 65, Application US/08981663  
; Patent No. 5952176  
; GENERAL INFORMATION:  
; APPLICANT: MCCARTHY, THOMAS VALENTINE  
; APPLICANT: VAUGHAN, PATRICK MARTIN  
; TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AT CANDIDATE LOCI  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

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;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/981.663
;; FILING DATE: 08-JAN-1998
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SVENSSON, LEONARD R.
;; REGISTRATION NUMBER: 30,330
;; REFERENCE/DOCKET NUMBER: 1377-120P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 205-8000
;; TELEFAX: (703) 205-8050
;; TELEX: 248345
;; INFORMATION FOR SEQ ID NO: 65:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 76 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Mycobacterium tuberculosis
;; US-08-981-663-65

Query Match 21.9%; Score 18.6; DB 2; Length 76;
Best Local Similarity 51.2%; Pred. No. 1.7e+03;
Matches 21; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 21 GGGCUGGUUAAGGCGGCCCAAGUUGGAAGGCGCGCUUUGCU 61
Db 43 GGGCTGTTTGGCGGCCACTACGTGTTAGTCAGGATGCT 3

RESULT 12
US-08-981-663-66
; Sequence 66, Application US/08981663
; Patent No. 5952176
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, THOMAS VALENTINE
; APPLICANT: VAUGHAN, PATRICK MARTIN
; TITLE OF INVENTION: GLYCOSYLASE MEDIATED DETECTION OF
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AT CANDIDATE LOCI
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981.663
; FILING DATE: 08-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1377-120P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 base pairs
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;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: YES
;; ORIGINAL SOURCE:
;; ORGANISM: Mycobacterium tuberculosis
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: 12
;; OTHER INFORMATION: /mod_base= i
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: 22
;; OTHER INFORMATION: /mod_base= i
;; FEATURE:
;; NAME/KEY: modified_base
;; LOCATION: 25
;; OTHER INFORMATION: /mod_base= i
;; US-08-981-663-66

Query Match 21.9%; Score 18.6; DB 2; Length 76;
Best Local Similarity 58.5%; Pred. No. 1.7e+03;
Matches 24; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 21 GGGCUGGUUAAGGCGGCCCAAGUUGGAAGGCGCGCUUUGCU 61
Db 34 GGGCTGTTTGGCGGCCACUACUGGUGGACAGGAGCU 74

RESULT 13
US-08-109-037-22
; Sequence 22, Application 08/109037
; Patent No. 6093538
; GENERAL INFORMATION:
; APPLICANT: James J. Hogan, Diane L. McAllister,
; APPLICANT: Patricia Gordon, and Philip W. Hammond.
; TITLE OF INVENTION: NUCLEIC ACID PROBES
; TITLE OF INVENTION: TO UREAPLASMA
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/109,037
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 07/879,685
; FILING DATE: May 6, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 193/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-109-037-22
Query Match 21.6%; Score 18.4; DB 3; Length 43;
Best Local Similarity 46.4%; Pred. No. 1.6e+03;
Matches 13; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 49 AGGCGCUUGCUUGCUUGCUUGCUUGGAUG 76
Db 16 AGAGTGTGACTTCTGTGTGGGATG 43

RESULT 14
US-08-109-037-55
; Sequence 55, Application 08/109037
; Patent No. 6093538
; GENERAL INFORMATION:
; APPLICANT: James J. Hogan, Diane L. McAllister,
; APPLICANT: Patricia Gordon, and Philip W. Hammond.
; TITLE OF INVENTION: NUCLEIC ACID PROBES
; TITLE OF INVENTION: TO UREAPLASMA
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/109,037
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 07/879,685
; FILING DATE: May 6, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 193/121
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-109-037-55
Query Match 21.6%; Score 18.4; DB 3; Length 43;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 49 AGGCGCUUGCUUGCUUGCUUGCUUGGAUG 76
Db 16 AGAGUGCUUGACUUGCUUGCUUGGAUG 43

RESULT 15
US-08-109-037-56/c
; Sequence 56, Application 08/109037

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; Patent No. 6093538
; GENERAL INFORMATION:
; APPLICANT: James J. Hogan, Diane L. McAllister,
; APPLICANT: Patricia Gordon, and Philip W. Hammond.
; TITLE OF INVENTION: NUCLEIC ACID PROBES
; TITLE OF INVENTION: TO UREAPLASMA
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/109,037
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 07/879,685
; FILING DATE: May 6, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 193/121
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-109-037-56
Query Match 21.6%; Score 18.4; DB 3; Length 43;
Best Local Similarity 46.4%; Pred. No. 1.6e+03;
Matches 13; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 49 AGGCGCUUGCUUGCUUGCUUGCUUGGAUG 76
Db 28 AGAGTGTGACTTCTGTGTGGGATG 1

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	3	20.2	23.8	66	11	US-10-310-914A-11123	Sequence 11123, A
	4	20.2	23.8	68	11	US-10-310-914A-13331	Sequence 13331, A
	5	20	23.5	60	3	US-09-908-975-9052	Sequence 9052, Ap
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C	7	19.2	22.6	65	3	US-09-908-975-26691	Sequence 26691, A
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	9	19.2	22.6	80	7	US-10-384-245-814	Sequence 814, App
	10	19	22.4	80	8	US-10-131-827-5504	Sequence 5504, Ap
	11	19	22.4	50	16	US-11-175-859-53521	Sequence 53521, A
	12	19	22.4	64	11	US-10-310-914A-10113	Sequence 10113, A
C	13	18.8	22.1	65	3	US-09-908-975-4025	Sequence 4025, Ap
	14	18.8	22.1	70	10	US-10-957-432-458	Sequence 458, App
	15	18.8	22.1	73	11	US-10-310-914A-11927	Sequence 11927, A
	16	18.8	22.1	83	11	US-10-310-914A-6916	Sequence 6916, Ap
	17	18.6	21.9	50	16	US-11-175-859-26823	Sequence 26823, A
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# Introduction

US-09-908-975-4025



us-10-604-726a-6033.sizlim85.rnpbm

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Fri Jun 22 07:29:32 2007

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

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- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq3.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq4.\*
- 17: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq5.\*
- 18: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq6.\*
- 19: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq7.\*
- 20: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq8.\*
- 21: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
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C 2	29	34.1	32	11	US-10-536-560-390712
C 3	21.4	25.2	50	7	US-10-990-275-2856
C 4	21.4	25.2	50	7	US-10-990-298-2856
C 5	21.4	25.2	50	8	US-10-006-290-2856
C 6	21.4	25.2	50	11	US-10-325-899-2856
C 7	20.8	24.5	64	19	US-11-130-645A-423399
C 8	20.8	24.5	64	19	US-11-130-645A-543086
C 9	20.6	24.2	62	19	US-11-130-645A-57160
C 10	20.6	24.2	63	19	US-11-130-645A-341409
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12	20.2	23.8	64	19	US-11-130-645A-275352	Sequence 275352,
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14	20.2	23.8	64	19	US-11-130-645A-520800	Sequence 520800,
15	20.2	23.8	64	19	US-11-130-645A-618491	Sequence 618491,
16	20.2	23.8	64	19	US-11-130-645A-695355	Sequence 695355,
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18	20	23.5	64	19	US-11-130-645A-103744	Sequence 103744,
19	20	23.5	64	19	US-11-130-645A-165356	Sequence 165356,
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21	19.8	23.3	64	19	US-11-130-645A-671551	Sequence 671551,
22	19.6	23.3	83	11	US-10-664-025-13389	Sequence 13389, A
23	19.6	23.1	60	18	US-11-454-157-529	Sequence 529, App
24	19.6	23.1	64	19	US-11-130-645A-106591	Sequence 106591,
25	19.6	23.1	64	19	US-11-130-645A-609590	Sequence 609590,
26	19.6	23.1	83	20	US-11-503-243A-424753	Sequence 424753,
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28	19.4	22.8	64	19	US-11-130-645A-121298	Sequence 121298,
29	19.4	22.8	64	19	US-11-130-645A-456321	Sequence 456321,
30	19.4	22.8	64	19	US-11-130-645A-457656	Sequence 457656,
31	19.4	22.8	64	19	US-11-130-645A-570264	Sequence 570264,
32	19.4	22.8	66	19	US-11-130-645A-456777	Sequence 456777,
33	19.2	22.6	64	19	US-11-130-645A-97233	Sequence 97233, A
34	19.2	22.6	64	19	US-11-130-645A-641237	Sequence 641237,
35	19.2	22.6	65	19	US-11-130-645A-341772	Sequence 341772,
36	19.2	22.6	82	19	US-11-130-645A-3534	Sequence 3534, Ap
37	19	22.4	50	7	US-10-990-275-5504	Sequence 5504, Ap
38	19	22.4	50	7	US-10-990-298-5504	Sequence 5504, Ap
39	19	22.4	50	8	US-10-006-290-5504	Sequence 5504, Ap
40	19	22.4	50	11	US-10-325-899-5504	Sequence 5504, Ap
41	19	22.4	64	19	US-11-130-645A-68630	Sequence 68630, A
42	19	22.4	64	19	US-11-130-645A-413529	Sequence 413529,
43	19	22.4	64	19	US-11-130-645A-482237	Sequence 482237,
44	19	22.4	64	19	US-11-130-645A-657688	Sequence 657688,
45	19	22.4	64	19	US-11-130-645A-738447	Sequence 738447,

## ALIGNMENTS

RESULT 1  
US-10-536-560-175427/c  
; Sequence 175427, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY  
; TITLE OF INVENTION: GENES AND USES THEREOF  
; FILE REFERENCE: 06087.0300.PCUI3  
; CURRENT APPLICATION NUMBER: US/10/536.560  
; CURRENT FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 424571  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 175427  
; LENGTH: 32  
; TYPE: RNA  
; ORGANISM: Homo Sapiens  
US-10-536-560-175427

Query Match 37.6%; Score 32; DB 11; Length 32;  
Best Local Similarity 78.1%; Pred. No. 0.24;  
Matches 25; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 15 UGAGAGGGGCGUUAAGGCGGCCCAAGUUG 46  
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Db 32 TGAGAGGGGCGTGTAAAGGCGTCCCAAGTTG 1

RESULT 2  
US-10-536-560-390712/c  
; Sequence 390712, Application US/10536560  
; Publication No. US20060257851A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 06087.0300.PCUI3
; CURRENT APPLICATION NUMBER: US/10/536,560
; CURRENT FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 424571
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 390712
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-536-560-390712

Query Match. 34.1%; Score 29; DB 11; Length 32;
Best Local Similarity 55.2%; Pred. No. 2.9;
Matches 16; Conservative 13; Mismatches 0; Indels 0; Gaps 0;

Qy 57 UUGUUGUUUUUGGAGGAGGAGUCCU 85
Db 32 TTGCTTCTGTTTCTGGATGCAGAGTCCT 4

RESULT 3
US-10-990-275-2856
; Sequence 2856, Application US/10990275
; Publication No. US20070037166A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 50661200011
; CURRENT APPLICATION NUMBER: US/10/990,275
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2856
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-275-2856

Query Match 25.2%; Score 21.4; DB 7; Length 50;
Best Local Similarity 41.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

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Db 1 AGTCCCAAGGGTGTTTGTACTGTTTCTCCATGAATA 39

RESULT 4
US-10-990-298-2856
; Sequence 2856, Application US/10990298
; Publication No. US20070037167A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000110
; CURRENT APPLICATION NUMBER: US/10/990,298
; CURRENT FILING DATE: 2004-11-15

; PRIOR APPLICATION NUMBER: US 10/131,827
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2856
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-298-2856

Query Match 25.2%; Score 21.4; DB 7; Length 50;
Best Local Similarity 41.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGCGCUUGUCUUGUUUUGGAGGAGCAGA 80
Db 1 AGTCCCAAGGGTGTTTGTACTGTTTCTCCATGAATA 39

RESULT 5
US-10-006-290-2856
; Sequence 2856, Application US/10006290
; Publication No. US20070037144A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Quetermous, Thomas
; APPLICANT: Johnson, Frances
; APPLICANT: Fry, Kirk
; APPLICANT: Matcuk, George
; APPLICANT: Prentice, James
; APPLICANT: Phillips, Julie
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Altman, Peter
; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
; FILE REFERENCE: 506612000100
; CURRENT APPLICATION NUMBER: US/10/006,290
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/241,994
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 8832
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2856
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-290-2856

Query Match 25.2%; Score 21.4; DB 8; Length 50;
Best Local Similarity 41.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGCGCUUGUCUUGUUUUGGAGGAGCAGA 80
Db 1 AGTCCCAAGGGTGTTTGTACTGTTTCTCCATGAATA 39

RESULT 6
US-10-325-899-2856
; Sequence 2856, Application US/10325899
; Publication No. US20070031890A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Ly, Ngoc
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT

;; TITLE OF INVENTION: REJECTION  
;; FILE REFERENCE: 506612008122  
;; CURRENT APPLICATION NUMBER: US/10/325,899  
;; CURRENT FILING DATE: 2002-12-20  
;; PRIOR APPLICATION NUMBER: US 60/296,764  
;; PRIOR FILING DATE: 2001-06-08  
;; PRIOR APPLICATION NUMBER: US 10/006,290  
;; PRIOR FILING DATE: 2001-10-22  
;; PRIOR APPLICATION NUMBER: US 10/131,831  
;; PRIOR FILING DATE: 2002-04-24  
;; NUMBER OF SEQ ID NOS: 966  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 2856  
;; LENGTH: 50  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-325-899-2856

Query Match 25.2%; Score 21.4; DB 11; Length 50;  
Best Local Similarity 41.0%; Pred. No. 1.7e+03;  
Matches 16; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGCGUUGUUCUGUUGGAGCAGA 80  
Db 1 AGUUGAAGGCGUUGUUCUGUUGGAGCAGA 39

RESULT 7  
US-11-130-645A-423399  
; Sequence 423399, Application US/11130645A  
; Publication No. US20070050146A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Amir, Avniel  
; APPLICANT: Yael, Karov  
; APPLICANT: Ranit, Aharonov  
; TITLE OF INVENTION: Microtomas and Uses Thereof  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130,645A  
; CURRENT FILING DATE: 2005-05-16  
; PRIOR APPLICATION NUMBER: PCT/US05/16986  
; PRIOR FILING DATE: 2005-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,577  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,572  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 60/666,340  
; PRIOR FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: US 60/665,094  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/662,742  
; PRIOR FILING DATE: 2005-03-17  
; PRIOR APPLICATION NUMBER: US 60/593,329  
; PRIOR FILING DATE: 2005-01-06  
; PRIOR APPLICATION NUMBER: US 60/593,081  
; PRIOR FILING DATE: 2004-12-08  
; PRIOR APPLICATION NUMBER: US 60/522,860  
; PRIOR FILING DATE: 2004-11-15  
; PRIOR APPLICATION NUMBER: US 60/522,457  
; PRIOR FILING DATE: 2004-10-04  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 760616  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 423399  
; LENGTH: 64  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-130-645A-423399

Query Match 24.5%; Score 20.8; DB 19; Length 64;  
Best Local Similarity 60.7%; Pred. No. 2.9e+03;  
Matches 34; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 19 AGGGGCGUGUUAAGGCGUCCCAAGUGGAGGGCGUUGUUCUGUUGUUGGGA 74  
Db 1 AGGGGCGUGUUAAGGCGUCCCAAGUGGAGGGCGUUGUUCUGUUGUUGGGA 56

RESULT 8  
US-11-130-645A-543086  
; Sequence 543086, Application US/11130645A  
; Publication No. US20070050146A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Amir, Avniel  
; APPLICANT: Yael, Karov  
; APPLICANT: Ranit, Aharonov  
; TITLE OF INVENTION: Microtomas and Uses Thereof  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130,645A  
; CURRENT FILING DATE: 2005-05-16  
; PRIOR APPLICATION NUMBER: PCT/US05/16986  
; PRIOR FILING DATE: 2005-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,577  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,572  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 60/666,340  
; PRIOR FILING DATE: 2005-03-30  
; PRIOR APPLICATION NUMBER: US 60/665,094  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/662,742  
; PRIOR FILING DATE: 2005-03-17  
; PRIOR APPLICATION NUMBER: US 60/593,329  
; PRIOR FILING DATE: 2005-01-06  
; PRIOR APPLICATION NUMBER: US 60/593,081  
; PRIOR FILING DATE: 2004-12-08  
; PRIOR APPLICATION NUMBER: US 60/522,860  
; PRIOR FILING DATE: 2004-11-15  
; PRIOR APPLICATION NUMBER: US 60/522,457  
; PRIOR FILING DATE: 2004-10-04  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 760616  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 543086  
; LENGTH: 64  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-130-645A-543086

Query Match 24.5%; Score 20.8; DB 19; Length 64;  
Best Local Similarity 60.7%; Pred. No. 2.9e+03;  
Matches 34; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 19 AGGGGCGUGUUAAGGCGUCCCAAGUGGAGGGCGUUGUUCUGUUGUUGGGA 74  
Db 1 AGGGGCGUGUUAAGGCGUCCCAAGUGGAGGGCGUUGUUCUGUUGUUGGGA 56

RESULT 9  
US-11-130-645A-57160  
; Sequence 57160, Application US/11130645A  
; Publication No. US20070050146A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Amir, Avniel  
; APPLICANT: Yael, Karov  
; APPLICANT: Ranit, Aharonov  
; TITLE OF INVENTION: Microtomas and Uses Thereof  
; FILE REFERENCE: 06087.0202.CPUS13  
; CURRENT APPLICATION NUMBER: US/11/130,645A  
; CURRENT FILING DATE: 2005-05-16  
; PRIOR APPLICATION NUMBER: PCT/US05/16986  
; PRIOR FILING DATE: 2005-05-14  
; PRIOR APPLICATION NUMBER: US 10/709,577  
; PRIOR FILING DATE: 2004-05-14

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; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 57160
; LENGTH: 62
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-57160

Query Match      24.2%; Score 20.6; DB 19; Length 62;
Best Local Similarity 67.4%; Pred. No. 3.4e+03;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 3 GUUAUUGCAACUGAGAGGGGCGUGGUUAAGCGUCCCAAGUU 45
Db 17 GUGAUAAGAAACUUUGAAGGCGUAUUUAUCGCGUCCCAAGUU 59

RESULT 10
US-11-130-645A-341409
; Sequence 341409, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; TITLE OF INVENTION: Micronas and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 341409
; LENGTH: 63
; TYPE: RNA
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; ORGANISM: Homo sapiens
US-11-130-645A-341409

Query Match      24.2%; Score 20.6; DB 19; Length 63;
Best Local Similarity 67.4%; Pred. No. 3.4e+03;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 2 GUUAUUGCAACUGAGAGGGGCGUGGUUAAGCGUCCCAAGU 44
Db 1 GUUCAUCCAGACAGACAGAGUGUGGUUACAGCGCCCUCAGU 43

RESULT 11
US-11-130-645A-175103
; Sequence 175103, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; TITLE OF INVENTION: Micronas and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130,645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 175103
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-175103

Query Match      23.8%; Score 20.2; DB 19; Length 64;
Best Local Similarity 75.8%; Pred. No. 4.7e+03;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGCGCGUUGCUUGCUUUUUUCUGGA 74
Db 7 AUUUGAAUAAGGAUUUGGCUUUUUUCUGGA 39

RESULT 12
US-11-130-645A-275352
; Sequence 275352, Application US/11130645A
; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; TITLE OF INVENTION: Micronas and Uses Thereof
```

FILE REFERENCE: 06087.0202.CPUS13  
CURRENT APPLICATION NUMBER: US/11/130.645A  
CURRENT FILING DATE: 2005-05-16  
PRIOR APPLICATION NUMBER: PCT/US05/16986  
PRIOR FILING DATE: 2005-05-14  
PRIOR APPLICATION NUMBER: US 10/709,577  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 10/709,572  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 60/666,340  
PRIOR FILING DATE: 2005-03-30  
PRIOR APPLICATION NUMBER: US 60/665,094  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/662,742  
PRIOR FILING DATE: 2005-03-17  
PRIOR APPLICATION NUMBER: US 60/593,329  
PRIOR FILING DATE: 2005-01-06  
PRIOR APPLICATION NUMBER: US 60/593,081  
PRIOR FILING DATE: 2004-12-08  
PRIOR APPLICATION NUMBER: US 60/522,860  
PRIOR FILING DATE: 2004-11-15  
PRIOR APPLICATION NUMBER: US 60/522,457  
PRIOR FILING DATE: 2004-10-04  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 760616  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 275352  
LENGTH: 64  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-130-645A-275352

Query Match 23.8%; Score 20.2; DB 19; Length 64;  
Best Local Similarity 75.8%; Pred. No. 4.7e+03;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGGCGGCUUUGCUUUCUGUUGGA 74  
|||||  
Db 6 AUUUGAAUAAGGAUUGGCUUUCUGGA 38

RESULT 13  
US-11-130-645A-518054  
Sequence 518054, Application US/11130645A  
Publication No. US20070050146A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Itzhak  
APPLICANT: Amir, Avniel  
APPLICANT: Yael, Karov  
APPLICANT: Ranit, Aharonov  
TITLE OF INVENTION: Microtnas and Uses Thereof  
FILE REFERENCE: 06087.0202.CPUS13  
CURRENT APPLICATION NUMBER: US/11/130.645A  
CURRENT FILING DATE: 2005-05-16  
PRIOR APPLICATION NUMBER: PCT/US05/16986  
PRIOR FILING DATE: 2005-05-14  
PRIOR APPLICATION NUMBER: US 10/709,577  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 10/709,572  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 60/666,340  
PRIOR FILING DATE: 2005-03-30  
PRIOR APPLICATION NUMBER: US 60/665,094  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/662,742  
PRIOR FILING DATE: 2005-03-17  
PRIOR APPLICATION NUMBER: US 60/593,329  
PRIOR FILING DATE: 2005-01-06  
PRIOR APPLICATION NUMBER: US 60/593,081  
PRIOR FILING DATE: 2004-12-08  
PRIOR APPLICATION NUMBER: US 60/522,860  
PRIOR FILING DATE: 2004-11-15  
PRIOR APPLICATION NUMBER: US 60/522,457

PRIOR FILING DATE: 2004-10-04  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 760616  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 518054  
LENGTH: 64  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-130-645A-518054

Query Match 23.8%; Score 20.2; DB 19; Length 64;  
Best Local Similarity 75.8%; Pred. No. 4.7e+03;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 42 AGUUGAAGGGCGGCUUUGCUUUCUGUUGGA 74  
|||||  
Db 6 AUUUGAAUAAGGAUUGGCUUUCUGGA 38

RESULT 14  
US-11-130-645A-520800  
Sequence 520800, Application US/11130645A  
Publication No. US20070050146A1  
GENERAL INFORMATION:  
APPLICANT: Bentwich, Itzhak  
APPLICANT: Amir, Avniel  
APPLICANT: Yael, Karov  
APPLICANT: Ranit, Aharonov  
TITLE OF INVENTION: Microtnas and Uses Thereof  
FILE REFERENCE: 06087.0202.CPUS13  
CURRENT APPLICATION NUMBER: US/11/130.645A  
CURRENT FILING DATE: 2005-05-16  
PRIOR APPLICATION NUMBER: PCT/US05/16986  
PRIOR FILING DATE: 2005-05-14  
PRIOR APPLICATION NUMBER: US 10/709,577  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 10/709,572  
PRIOR FILING DATE: 2004-05-14  
PRIOR APPLICATION NUMBER: US 60/666,340  
PRIOR FILING DATE: 2005-03-30  
PRIOR APPLICATION NUMBER: US 60/665,094  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/662,742  
PRIOR FILING DATE: 2005-03-17  
PRIOR APPLICATION NUMBER: US 60/593,329  
PRIOR FILING DATE: 2005-01-06  
PRIOR APPLICATION NUMBER: US 60/593,081  
PRIOR FILING DATE: 2004-12-08  
PRIOR APPLICATION NUMBER: US 60/522,860  
PRIOR FILING DATE: 2004-11-15  
PRIOR APPLICATION NUMBER: US 60/522,457  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 760616  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 520800  
LENGTH: 64  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-130-645A-520800

Query Match 23.8%; Score 20.2; DB 19; Length 64;  
Best Local Similarity 59.6%; Pred. No. 4.7e+03;  
Matches 34; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 12 AACUGAGAGGGCGGCUUUGAAGCGGCCCAAGUUGAAGGGCGCUUUCUGUUG 68  
|||||  
Db 1 AAAGAAGAGGGCGCAGCUUUGAUGGUGUUGAUGGAGUUGAUGGAGUUGUUGUCU 57

RESULT 15  
US-11-130-645A-618491  
Sequence 618491, Application US/11130645A

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; Publication No. US20070050146A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Itzhak
; APPLICANT: Amir, Avniel
; APPLICANT: Yael, Karov
; APPLICANT: Ranit, Aharonov
; TITLE OF INVENTION: MicroRNAs and Uses Thereof
; FILE REFERENCE: 06087.0202.CPUS13
; CURRENT APPLICATION NUMBER: US/11/130.645A
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: PCT/US05/16986
; PRIOR FILING DATE: 2005-05-14
; PRIOR APPLICATION NUMBER: US 10/709,577
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 10/709,572
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/666,340
; PRIOR FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US 60/665,094
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/662,742
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US 60/593,329
; PRIOR FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: US 60/593,081
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: US 60/522,860
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/522,457
; PRIOR FILING DATE: 2004-10-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 760616
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 618491
; LENGTH: 64
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-130-645A-618491

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Query Match      23.8%; Score 20.2; DB 19; Length 64;
Best Local Similarity 75.8%; Pred. No. 4.7e+03;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy      42 AGUUGGAAGCGCUCUUGCUUGUUUUCUGGA 74
Db      7 AUUUGAAUAGGAUUGGUCUUGUUUUCUGGA 39

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Search completed: June 19, 2007, 18:08:19  
Job time : 1268 secs

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 15:45:58 ; Search time 4740 Seconds  
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Title: US-10-604-726A-6033  
Perfect score: 85  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 709684

Minimum DB seq length: 0  
Maximum DB seq length: 85

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb\_est3.\*
- 3: gb\_est4.\*
- 4: gb\_est5.\*
- 5: gb\_est6.\*
- 6: gb\_est7.\*
- 7: gb\_est8.\*
- 8: gb\_est9.\*
- 9: gb\_est10.\*
- 10: gb\_est11.\*
- 11: gb\_est12.\*
- 12: gb\_est13.\*
- 13: gb\_est14.\*
- 14: gb\_est15.\*
- 15: gb\_est16.\*
- 16: gb\_est17.\*
- 17: gb\_est18.\*
- 18: gb\_est19.\*
- 19: gb\_est20.\*

Pred..No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.8	25.6	81	11	EC651791
2	21.2	24.9	64	19	BX947927 Arabidops
3	21	24.7	73	12	DY796917 PMAL-aa5
C 4	20.4	24.0	77	7	AV858990 AV858990
C 5	20.2	23.8	82	13	DN496082
6	20	23.5	81	12	EB927323 12064370
7	19.8	23.3	76	19	CRO24485 Forward s
8	19.6	23.1	81	6	AK197638 Mus muscu
9	19.6	23.1	84	4	BU865564 S055D05 P
C 10	19.4	22.8	68	19	DQ041030 Pan trogl
11	19.4	22.8	79	1	AA619735 v160c06.s
12	19.4	22.8	85	10	CN869173
C 13	19.2	22.6	58	1	AI423081 tf18b11.x
14	19	22.4	55	3	BI408546 602963185

C 15	19	22.4	65	16	BZ592639
16	19	22.4	70	14	CX296360
17	19	22.4	74	17	CG646686
18	19	22.4	81	15	BH416654
C 19	18.8	22.1	69	10	CV294687
C 20	18.8	22.1	73	15	AZ784729
21	18.8	22.1	75	19	CR161283
C 22	18.8	22.1	84	2	BF531086
C 23	18.8	22.1	84	19	BX003952
C 24	18.6	21.9	44	2	BF102281
25	18.6	21.9	61	15	AZ918852
C 26	18.6	21.9	63	7	AU255617
27	18.6	21.9	76	1	AI943197
C 28	18.6	21.9	76	5	C00941
C 29	18.6	21.9	80	11	EC620703
C 30	18.4	21.6	50	16	BH861963
C 31	18.4	21.6	65	10	CT685647
C 32	18.4	21.6	71	12	EB421640
C 33	18.4	21.6	76	11	EC732719
34	18.4	21.6	78	9	CK125805
35	18.4	21.6	81	5	CA833496
36	18.4	21.6	83	11	EC782505
C 37	18.4	21.6	84	3	BI828236
C 38	18.4	21.6	84	12	EB423837
C 39	18.2	21.4	63	10	CV583912
C 40	18.2	21.4	81	15	AZ388677
41	18.2	21.4	83	1	AI873146
C 42	18.2	21.4	83	8	CP453329
43	18.2	21.4	84	3	BM433199
44	18	21.2	50	7	AU106784
45	18	21.2	67	15	AZ804828

## ALIGNMENTS

RESULT 1	EC651791	EC651791	81 bp	mRNA	linear	EST 29-JUN-2006
LOCUS	EC651791	CD300009311	Cyanophora paradoxa	High light	Cyanophora paradoxa	
DEFINITION	CDNA, mRNA sequence.					
ACCESSION	EC651791					
VERSION	EC651791.1	GI:109759395				
KEYWORDS	EST.					
SOURCE	Cyanophora paradoxa					
ORGANISM	Cyanophora paradoxa					
REFERENCE	1 (bases 1 to 81)					
AUTHORS	Durnford,D.G.					
TITLE	TBestDB [http://tbestdb.bcm.umontreal.ca/searches/login.php]					
JOURNAL	Cyanophora paradoxa [Durnford lab]					
COMMENT	Unpublished (2006)					
	Contact: TBestDB					
	Département de Biochimie, Université de Montréal					
	Montreal, Canada					
	Email: tbestdb-curator@bch.umontreal.ca					
	Plate: 2571.					
FEATURES	Location/Qualifiers					
source	1..81					
	/organism="Cyanophora paradoxa"					
	/mol_type="mRNA"					
	/db_xref="taxon:2762"					
	/clone_lib="Cyanophora paradoxa High light"					
	/note="Durnford lab"					
ORIGIN						
Query Match	25.6%;	Score 21.8;	DB 11;	Length 81;		
Best Local Similarity	40.8%;	Pred. No. 2.3e+04;				
Matches	20;	Conservative 12;	Mismatches 17;	Indels 0;	Gaps 0;	
Qy	23	CGUGUUAAGCGGCCCAAGUAGAGGGCGCUUUGCUUGUUCU 71				
Db	3	GCTGTTGTCGCGCACCCAGTTCGTCGCTCATTCCAACTCTTCT 51				



```

RESULT 2
LOCUS      BX947927                64 bp    DNA        linear    GSS 05-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-785G09-024929,
            genomic survey sequence.
ACCESSION  BX947927
VERSION    BX947927.1  GI:42597613
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
REFERENCE  1
AUTHORS    Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE      GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
JOURNAL    Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED    12874060
REFERENCE  2
AUTHORS    Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
            Weisshaar,B.
TITLE      High-throughput generation of sequence indexes from T-DNA
            mutagenized Arabidopsis thaliana lines
JOURNAL    Biotechniques 35 (6), 1164-1168 (2003)
PUBMED    14682050
REFERENCE  3
AUTHORS    Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.
TITLE      Direct Submission
JOURNAL    Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
            zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
            This sequence has been recovered from the left border of the T-DNA.
            It indicates an insertion close to or within gene At3g16050.
            Details on the protocols used for generation of the sequence are
            described in References 1-3. The sequences are generated at the MPI
            for Plant Breeding Research in the context of the GABI-Kat project.
            GABI-Kat is part of the German Plant Genomics program designated
            'GABI'. Information on line availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES   Location/Qualifiers
            1..64
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /db_xref="taxon:3702"
            /clone="GK-785G09-024929"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            /ecotype="Col-0"
            /note="PCR was performed on DNA from Arabidopsis thaliana
            plants (T1) which were transformed with the T-DNA from
            vector pAC161 (GenBank accession number: AJ537514). The
            lines contain one or more T-DNA insertions. The DNA
            fragment(s) resulting from the PCR were directly sequenced
            to determine the genomic sequence flanking the insertion.
            T-DNA derived sequences were removed."
ORIGIN
Query Match      24.9%; Score 21.2; DB 19; Length 64;
Best Local Similarity 40.5%; Pred. No. 3.5e+04;
Matches 17; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 36 UCCCAAGUAGGAGGCGCUUGUUCUGUUCUGGAGUC 77
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      TCTCATCATGAGGCCACTAGTTCTTTCTTCGTCATAC 48

Db

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```

RESULT 3
LOCUS      DY796917                73 bp    mRNA        linear    EST 21-MAR-2006
DEFINITION PMAL-aa57b05.b1 Lamprey_EST_Tissues Petromyzon marinus cDNA 3',
            mRNA sequence.
ACCESSION  DY796917
VERSION    DY796917.1  GI:90141134
KEYWORDS   EST.
SOURCE     Petromyzon marinus (sea lamprey)
ORGANISM   Petromyzon marinus
REFERENCE  1
AUTHORS    Wilson,R.
TITLE      WashU Lamprey EST project
JOURNAL    Unpublished (2005)
COMMENT    Contact: Ziping Zhang
            WashU Lamprey EST project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: submissions@watson.wustl.edu
            Library material provided by Department of Fisheries & Wildlife,
            Michigan State University Library constructed by Ziping Zhang;
            Yilei Wang; Weiming Li Library sequenced by Washington University
            Genome Sequencing Center
            This trace has been recalled with phred
            original value before phred recall for SL was 0
            original value before phred recall for SR was 122
            Seq primer: pDNR-LIB-reverse.
FEATURES   Location/Qualifiers
            1..73
            /organism="Petromyzon marinus"
            /mol_type="mRNA"
            /db_xref="taxon:7757"
            /sex="Mix"
            /dev_stage="Adult"
            /lab_host="DH10B"
            /clone_lib="Lamprey EST Tissues"
            /note="Vector: pDNR-LIB; Site_1: Sfi I; Site_2: Sfi I"
ORIGIN
Query Match      24.7%; Score 21; DB 12; Length 73;
Best Local Similarity 40.5%; Pred. No. 4.2e+04;
Matches 15; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 49 AGGGCGCUUCUGUUCUGUUCUGGAGUCAGAGUCUCU 85
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      21 AGGGTTTTTTTTTTTTTTTCTGCGATTCAGAGCCCT 57

Db

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RESULT 4
LOCUS      AV858990/c              77 bp    mRNA        linear    EST 08-NOV-2001
DEFINITION AV858990 Nori Satoh unpublished cDNA library, larva Ciona
            intestinalis cDNA clone rcilv21013 3', mRNA sequence.
ACCESSION  AV858990
VERSION    AV858990.1  GI:16846514
KEYWORDS   EST.
SOURCE     Ciona intestinalis
ORGANISM   Ciona intestinalis
REFERENCE  1
AUTHORS    Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE      Expressed genes in Ciona intestinalis
JOURNAL    Unpublished (2000)
COMMENT    Contact: Nori Satoh
            Department of Zoology
            Kyoto University

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ORIGIN
Query Match      23.3%; Score 19.8; DB 19; Length 76;
Best Local Similarity 36.6%; Pred. No. 1.1e+05;
Matches 26; Conservative 13; Mismatches 32; Indels 0; Gaps 0;

Qy 3 GUUAUCUGCAACGAGAGGCGUGUUAAGCGGUCCCAAGUUGAGGCGCUUUGCUU 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GTGCTAGGAACGAAGGCGGATGCTGATGGTTGGTAGCTAGCTAGGAACGCTGTTA 60

Qy 63 CUGUUUUCUGG 73
   |||:|||||:
Db 61 ATGTTTACTTG 71

RESULT 8
AKI197638
LOCUS
DEFINITION
Mus musculus cDNA, clone:Y1G0125L04, strand:minus,
reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000045844, based
on BLAT search.
ACCESSION
AKI197638.1 GI:56021815
VERSION
HTC; ASSETS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1
Watahiki,A., Waki,K., Hayatsu,N., Shiraki,T., Kondo,S.,
Nakamura,M., Sasaki,D., Akakawa,T., Kawai,J., Harbers,M.,
Hayashizaki,Y. and Carninci,P.
Hayashizaki,Y. and Carninci,P.
Libraries enriched for alternatively spliced exons reveal splicing
patterns in melanocytes and melanomas
Nat. Methods 1 (3), 233-239 (2004)
15782199
2 (bases 1 to 81)
Arakawa,T., Carninci,P., Fukuda,S., Harbers,M., Hayatsu,N.,
Hori,F., Imotani,K., Kawai,J., Kondo,S., Murata,M., Nakamura,M.,
Nomura,K., Ohno,M., Sasaki,D., Shiraki,T., Waki,K., Watahiki,A. and
Hayashizaki,Y.
Direct Submission
Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gscl.riken.jp,
URL:http://genome.gsc.riken.jp, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Alternative Splicing Libraries (ASLs) are prepared by: Preparing
of single-stranded DNA using a RNA template from full length cDNA
libraries, hybridizing of
single-stranded DNAs, removing of remaining single-stranded DNA,
digesting of regions comprising double-stranded DNA by a set of 4
bp cutters, capturing of DNA hybrids with loop structures
(alternative spliced exon), ligation of Y-shaped primers to
isolated DNA hybrids with loop structures, PCR amplification of
ligation products and their cloning into pFLCI vector. (Reference).
Location/Qualifiers
1. 81
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="Y1G0125L04"
/cell_line="mixture of B16-F10Y and melan-c"
/cell_type="mixture of melanoma cell and melanocyte cell"
/clone_lib="Alternative Splicing Library L1"
/note="strand:minus, reference:ENSEMBL:Mouse-Transcript-
ENST:ENSMUST0000045844, based on BLAT search"

FEATURES
source
1. 81

ORIGIN
Query Match      23.1%; Score 19.6; DB 6; Length 81;
Best Local Similarity 42.3%; Pred. No. 1.2e+05;
Matches 11; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 55 CUUUCUUCUGUUUUCUGAUCGACA 80
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 CTTTGTCTTTGCTTTCTGATTCGGA 34

RESULT 10
DQ041030/c
LOCUS
DEFINITION
Pan troglodytes HC7216 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
DQ041030
VERSION
DQ041030.1 GI:66892245
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
Catarrhini; Homnidae; Pan.
1 (bases 1 to 68)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Cividello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
Chimp PLoS Biol. 3 (6), E170 (2005)
15869325
REFERENCE
2 (bases 1 to 68)

```

**ORIGIN**

Query Match 22.8%; Score 19.4; DB 1; Length 79;  
Best Local Similarity 48.9%; Pred. No. 1.4e+05;  
Matches 22; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

**QY** 17 AGAGGGGUGUUAAGCGGUCCCAAGUUGAAGGCGGCUUCGU 61  
|||||::|||:|||||::|||:|||||:  
**Dd** 29 AGAGGAGGTGGTGAGGCACAAAGCAAGATTAGATGAAGAAGTTGCT 73  
|||||::|||:|||||::|||:|||||:

**RESULT 12**

CN869173 85 bp mRNA linear EST 03-JUN-2004  
LOCUS 001202AAOA004538HT (AAOA) Royal Gala phloem Malus x domestica cDNA  
DEFINITION clone AAOA004538, mRNA sequence.

ACCESSION CN869173  
VERSION CN869173.1 GI:48126779  
KEYWORDS EST.  
SOURCE Malus x domestica  
ORGANISM Malus x domestica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

**REFERENCE**

**AUTHORS** Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,  
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.,  
HortResearch Apple EST Project  
Unpublished (2004)  
Contact: Gleave,A.  
Sequencing Facility  
The Horticulture and Food Research Institute of New Zealand Ltd  
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand  
Tel.: 00 64 09 815 4200  
Fax: 00 64 09 815 4201  
Email: est@hortresearch.co.nz.

**TITLE** Location/Qualifiers  
**JOURNAL** 1..85  
**COMMENT** /organism="Malus x domestica"  
/mol\_type="mRNA"  
/db\_xref="taxon:3750"  
/clone="AAOA004538"  
/tissue\_type="Phloem", scrapings from inside of bark mature wood"  
/clone\_lib="(AAOA) Royal Gala phloem"  
/note="Vector: pBluescript SK(-); Library sequenced by Genesis Research & Development"

**FEATURES**

source 1..85

**ORIGIN**

Query Match 22.8%; Score 19.4; DB 10; Length 85;  
Best Local Similarity 53.3%; Pred. No. 1.5e+05;  
Matches 24; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

**QY** 12 AACUGAGAGGCGUGUUUAGGCGUCCCCCAAGUUGAAGGCGGU 56  
|||||::|||:|||||::|||:|||||:  
**Dd** 16 AACTTCGAGAGAAAACCTCAGCCCTCTCAAGATGGAAGGAGT 60  
|||||::|||:|||||::|||:|||||:

**RESULT 13**

AI423081/c 58 bp mRNA linear EST 28-MAR-1999  
LOCUS tf1db11.x1 NCI CGAP Brn23 Homo sapiens cDNA IMAGE:2096541 3', mRNA  
DEFINITION similar to TR:Q15214 Q15214 SALIVARY PROLINE-RICH PROTEIN 1 , mRNA  
sequence.

ACCESSION AI423081  
VERSION AI423081.1 GI:4269012  
KEYWORDS EST.



TDNA. This sequence lies within an annotated exon of At5g65210.

Class: TDNA tagged.

Location/Qualifiers

FEATURES

source

1..65  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_028210.16.80.n"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN

Query Match 22.4%; Score 19; DB 16; Length 65;  
 Best Local Similarity 50.0%; Pred. No. 1.9e+05;  
 Matches 18; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 4 UUAUCUGCAACUGAGAGCGGCGUGGUUAAGCGGUCCC 39  
 :: : || || || || || || || || || || || || || || ||  
 Db 48 TTNTGTGCCACCGAGAGAGTTGGTATATGCGTACC 13

Search completed: June 19, 2007, 17:47:05  
 Job time : 4746 secs

GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:41:00 ; Search time 1106 Seconds  
(without alignments)  
1499,898 Million cell updates/sec

Title: US-10-604-726A-6034  
Perfect score: 24  
Sequence: 1 ugagagggcgguuaagcgucc 24

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 2038054

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: GenEmbl.\*  
1: gb\_env.\*  
2: gb\_pat.\*  
3: gb\_ph.\*  
4: gb\_pl.\*  
5: gb\_pr.\*  
6: gb\_ro.\*  
7: gb\_sts.\*  
8: gb\_sy.\*  
9: gb\_un.\*  
10: gb\_vi.\*  
11: gb\_ov.\*  
12: gb\_htg.\*  
13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15.8	65.8	24	2	AX443910	Sequence
2	15.8	65.8	25	2	AX447886	Sequence
C 3	14.6	60.8	24	2	DD122759	NUCLEAR H
C 4	14.6	60.8	24	2	AX538707	Sequence
C 5	14.4	60.0	21	2	BD353840	Method of
C 6	13.8	57.5	22	2	AR036420	Sequence
C 7	13.8	57.5	22	2	I29861	Sequence 12
C 8	13.2	55.0	25	2	AR148541	Sequence
C 9	13.2	55.0	25	2	I62320	Sequence 23
C 10	13	54.2	17	2	BD379515	Method an
C 11	13	54.2	17	2	BD379516	Method an
C 12	13	54.2	17	2	BD379517	Method an
C 13	13	54.2	17	2	BD379518	Method an
C 14	13	54.2	17	2	AX215297	Sequence
C 15	13	54.2	17	2	AX215298	Sequence
C 16	13	54.2	17	2	AX215299	Sequence
C 17	13	54.2	17	2	AX215300	Sequence
C 18	13	54.2	20	2	BD405918	GENE AND

C 19	13	54.2	20	2	AX298773	Sequence
C 20	12.8	53.3	19	2	AR069252	Sequence
C 21	12.8	53.3	19	2	CS101953	Sequence
C 22	12.8	53.3	19	2	CS102090	Sequence
C 23	12.8	53.3	24	6	DQ755439	Rattus no
C 24	12.8	53.3	25	2	AR240243	Sequence
C 25	12.6	52.5	19	2	AR628705	Sequence
C 26	12.6	52.5	20	2	AR100388	Sequence
C 27	12.6	52.5	20	2	AR150043	Sequence
C 28	12.6	52.5	20	2	BD227916	Antigense
C 29	12.6	52.5	20	2	BD278694	Oligonucle
C 30	12.6	52.5	20	2	AR442443	Sequence
C 31	12.6	52.5	20	8	AB213914	Synthetic
C 32	12.6	52.5	21	2	AR231257	Sequence
C 33	12.6	52.5	22	2	BD301800	Pollinosi
C 34	12.6	52.5	22	2	CS020856	Sequence
C 35	12.6	52.5	25	2	AR404657	Sequence
C 36	12.4	51.7	20	2	BD272896	Control o
C 37	12.4	51.7	20	2	DD136913	A Pharmac
C 38	12.4	51.7	21	2	DD271504	Methods t
C 39	12.4	51.7	21	2	DD271505	Methods t
C 40	12.4	51.7	21	2	DD271506	Methods t
C 41	12.4	51.7	22	2	DD027364	Synthetic
C 42	12.4	51.7	24	2	AR151401	Sequence
C 43	12.4	51.7	24	2	CQ816772	Sequence
C 44	12.4	51.7	24	2	AX443802	Sequence
C 45	12.4	51.7	25	2	AX447783	Sequence

## ALIGNMENTS

RESULT 1	AX443910	AX443910	24 bp	DNA	linear	PAT 03-JUL-2002
LOCUS	Sequence 365 from Patent WO0216649.					
DEFINITION	AX443910					
ACCESSION	AX443910.1	GI:21691188				
VERSION						
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	other sequences; artificial sequences.					
REFERENCE	1					
AUTHORS	Gunderson,K.					
TITLE	Probes and decoder oligonucleotides					
JOURNAL	Patent: WO 0216649-A 365 28-FEB-2002;					
ILLUMINA, INC. (US)						
FEATURES	Location/Qualifiers					
source	1..24					
	/organism="synthetic construct"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:32630"					
	/note="Computer Generated Probe Sequence."					

ORIGIN						
Query Match	65.8%;	Score 15.8;	DB 2;	Length 24;		
Best Local Similarity	73.7%;	Pred. No. 6.8e+04;				
Matches 14;	Conservative 3;	Mismatches 2;	Indels 0;	Gaps 0;		
Qy	2	GAGAGGGCGGUGUAAGGC 20				
Db	4	GAGAGGGCGTGGTTAAGGC 22				
RESULT 2	AX447886	AX447886	25 bp	DNA	linear	PAT 03-JUL-2002
LOCUS	Sequence 4341 from Patent WO0216649.					
DEFINITION	AX447886					
ACCESSION	AX447886.1	GI:21696785				
VERSION						
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	synthetic construct					

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 4341 28-FEB-2002;
Illumina, Inc. (US)
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Query Match 65.8%; Score 15.8; DB 2; Length 25;
Best Local Similarity 73.7%; Pred. No. 6.7e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GAGAGGGCGUGUUAAGGC 20
||||| : : : : :
Db 5 GAGAGGGCGTTGTTAAGGC 23

RESULT 3
DD122759/c 24 bp DNA linear PAT 04-NOV-2005
LOCUS DD122759 NUCLEAR HORMONE RECEPTOR LIGAND BINDING DOMAIN.
DEFINITION DD122759
ACCESSION DD122759
VERSION DD122759.1 GI:92809446
KEYWORDS JP 2005500010-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Pierron,V.N., Allen,J.M., Allen,K.E., Phillips,T., Phelps,C.B.,
Fagan,R.J. and Potter,S.J.
TITLE NUCLEAR HORMONE RECEPTOR LIGAND BINDING DOMAIN
JOURNAL Patent: JP 2005500010-A 4 06-JAN-2005;
INPHARMATICA LIMITED
COMMENT OS Artificial Sequence
PN JP 2005500010-A/4
PD 06-JAN-2005
PR 05-MAR-2002 JP 2002569876
PR 05-MAR-2001 GB 0105402.2
PI valerie nathalie pierron,janet marjorie allen,kathryn PI
elizabeth allen,
PI tom phillips,christopher benjamin phelps,richard joseph fagan,
PI sarah jane potter
CC LBDG3 Reverse primer
FH Key Location/Qualifiers.
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 60.8%; Score 14.6; DB 2; Length 24;
Best Local Similarity 61.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 3 AGAGGGCGUGUUAAGCGUC 23
||||| : : : : :
Db 23 AGAGGGCGTTTAACTCGTC 3

RESULT 4
AX538707/c 24 bp DNA linear PAT 23-NOV-2002
LOCUS AX538707
DEFINITION AX538707
ACCESSION AX538707
VERSION AX538707.1 GI:25271321
KEYWORDS
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 4341 28-FEB-2002;
Illumina, Inc. (US)
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/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
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Query Match 65.8%; Score 15.8; DB 2; Length 25;
Best Local Similarity 73.7%; Pred. No. 6.7e+04;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GAGAGGGCGUGUUAAGGC 20
||||| : : : : :
Db 5 GAGAGGGCGTTGTTAAGGC 23

RESULT 3
DD122759/c 24 bp DNA linear PAT 04-NOV-2005
LOCUS DD122759 NUCLEAR HORMONE RECEPTOR LIGAND BINDING DOMAIN.
DEFINITION DD122759
ACCESSION DD122759
VERSION DD122759.1 GI:92809446
KEYWORDS JP 2005500010-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Pierron,V.N., Allen,J.M., Allen,K.E., Phillips,T., Phelps,C.B.,
Fagan,R.J. and Potter,S.J.
TITLE NUCLEAR HORMONE RECEPTOR LIGAND BINDING DOMAIN
JOURNAL Patent: JP 2005500010-A 4 06-JAN-2005;
INPHARMATICA LIMITED
COMMENT OS Artificial Sequence
PN JP 2005500010-A/4
PD 06-JAN-2005
PR 05-MAR-2002 JP 2002569876
PR 05-MAR-2001 GB 0105402.2
PI valerie nathalie pierron,janet marjorie allen,kathryn PI
elizabeth allen,
PI tom phillips,christopher benjamin phelps,richard joseph fagan,
PI sarah jane potter
CC LBDG3 Reverse primer
FH Key Location/Qualifiers.
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/db_xref="taxon:32630"
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Best Local Similarity 61.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 3 AGAGGGCGUGUUAAGCGUC 23
||||| : : : : :
Db 23 AGAGGGCGTTTAACTCGTC 3

RESULT 4
AX538707/c 24 bp DNA linear PAT 23-NOV-2002
LOCUS AX538707
DEFINITION AX538707
ACCESSION AX538707
VERSION AX538707.1 GI:25271321
KEYWORDS
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Fagan,R.J., Phelps,C.B., Phillips,T., Pierron,V.N., Allen,K.E.,
Allen,J.M. and Potter,S.J.
TITLE Nuclear hormone receptor ligand binding domain
JOURNAL Patent: WO 02070557-A 6 12-SEP-2002;
Inpharmatica Limited (GB)
FEATURES
source
1. .24
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="LBDG3 Reverse primer"
ORIGIN
Query Match 60.8%; Score 14.6; DB 2; Length 24;
Best Local Similarity 61.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 3 AGAGGGCGUGUUAAGCGUC 23
||||| : : : : :
Db 23 AGAGGGCGTTTAACTCGTC 3

RESULT 5
BD353840/c 21 bp DNA linear PAT 04-NOV-2005
LOCUS BD353840
DEFINITION Method of food analysis.
ACCESSION BD353840
VERSION BD353840.1 GI:92254966
KEYWORDS WO 03068964-A/7.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Yamakawa,H., Suzuki,E., Miyatake,K. and Hayakawa,K.
TITLE Method of food analysis
JOURNAL Patent: WO 03068964-A 7 21-AUG-2003;
H YAMAKAWA et al
COMMENT OS Artificial Sequence
PN WO 03068964-A/7
PD 21-AUG-2003
PR 26-SEP-2002 WO 2002JP009982
PR 15-FEB-2002 JP 02P 038930
PI hirohito yamakawa,eriko suzuki,kiyoko miyatake,katsuyuki PI
hayakawa
CC FAG19, designed sense primer based on 11 between 1464 and 1484
FH Key Location/Qualifiers.
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 60.0%; Score 14.4; DB 2; Length 21;
Best Local Similarity 68.8%; Pred. No. 3.2e+05;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GGGCGUGUUAAGCGUC 22
||||| : : : : :
Db 17 GGGCTGTTATGCGCT 2

RESULT 6
AR036420/c 22 bp DNA linear PAT 29-SEP-1999
LOCUS AR036420
DEFINITION Sequence 12 from patent US 5872214.
ACCESSION AR036420
VERSION AR036420.1 GI:5953088
KEYWORDS

```



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SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 22)
AUTHORS      Seizinger,B.R., Kley,N.A. and Bianchi,A.B.
TITLE        NF2 isoforms
JOURNAL      Patent: US 5872214-A 12 16-FEB-1999;
FEATURES     Location/Qualifiers
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Best Local Similarity 70.6%; Pred. No. 6e+05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAGGGCGUGUUAAGG 19
Db 17 AGAGGAGCTGGTTCAGG 1

RESULT 7
LOCUS      I29861          22 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 12 from patent US 5578462.
ACCESSION  I29861
VERSION     I29861.1 GI:1820652
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Seizinger,B.R., Kley,N.A. and Bianchi,A.B.
TITLE      NF2 isoforms
JOURNAL    Patent: US 5578462-A 12 26-NOV-1996;
FEATURES   Location/Qualifiers
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Query Match      57.5%; Score 13.8; DB 2; Length 22;
Best Local Similarity 70.6%; Pred. No. 6e+05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAGGGCGUGUUAAGG 19
Db 17 AGAGGAGCTGGTTCAGG 1

RESULT 8
LOCUS      AR148541/c     25 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 23 from patent US 6225115.
ACCESSION  AR148541
VERSION     AR148541.1 GI:15112631
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Smith,K.E., Borden,L.A., Weinshank,R.L. and Hartig,P.R.
TITLE      DNA encoding taurine and GABA transporters and uses thereof
JOURNAL    Patent: US 6225115-A 23 01-MAY-2001;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      55.0%; Score 13.2; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.1e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAGGGCGUGUUAAGG 19
Db 17 AGAGGAGCTGGTTCAGG 1

RESULT 9
LOCUS      I62320          25 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 23 from patent US 5658786.
ACCESSION  I62320
VERSION     I62320.1 GI:2480268
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Smith,K.E., Weinshank,R.L., Borden,L.A. and Hartig,P.R.
TITLE      DNA encoding rat taurine transporter and uses thereof
JOURNAL    Patent: US 5658786-A 23 19-AUG-1997;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      55.0%; Score 13.2; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.1e+06;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AGGGCGUGUUAAGCGU 22
Db 23 AGGTGCTGGTGAAGGCAT 6

RESULT 10
LOCUS      BD379515/c     17 bp      RNA      linear      PAT 04-NOV-2005
DEFINITION Method and Reagent for the Modulation and Diagnosis of CD20 and
              NOGO Gene Expression.
ACCESSION  BD379515
VERSION     BD379515.1 GI:92278608
KEYWORDS    JP 2003525037-A/739.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Blatt,L., Mcswiggen,J., Chorlila,B.M. and Harbali,P.
TITLE       Method and Reagent for the Modulation and Diagnosis of CD20 and
              NOGO Gene Expression
JOURNAL     Patent: JP 2003525037-A 739 26-AUG-2003;
              Ribozyme Pharmaceuticals Inc
              OS Artificial Sequence
              PN JP 2003525037-A/739
              PD 26-AUG-2003
              PF 09-FEB-2001 JP 2001558241
              PR 11-FEB-2000 US 60/181797,28-FEB-2000 US 60/185516, PR
              06-MAR-2000 US 60/187128
              PI Lawrence blatt,james mcswiggen,blatto m chorlila,peter pi
              harbali
              CC Description of Artificial Sequence: Nucleic Acid FH Key
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ORIGIN
Query Match      54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGCGUGUUAAGCGU 22
Db 23 AGGTGCTGGTGAAGGCAT 6

RESULT 11
LOCUS      BD379515/c     17 bp      RNA      linear      PAT 04-NOV-2005
DEFINITION Method and Reagent for the Modulation and Diagnosis of CD20 and
              NOGO Gene Expression.
ACCESSION  BD379515
VERSION     BD379515.1 GI:92278608
KEYWORDS    JP 2003525037-A/739.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Blatt,L., Mcswiggen,J., Chorlila,B.M. and Harbali,P.
TITLE       Method and Reagent for the Modulation and Diagnosis of CD20 and
              NOGO Gene Expression
JOURNAL     Patent: JP 2003525037-A 739 26-AUG-2003;
              Ribozyme Pharmaceuticals Inc
              OS Artificial Sequence
              PN JP 2003525037-A/739
              PD 26-AUG-2003
              PF 09-FEB-2001 JP 2001558241
              PR 11-FEB-2000 US 60/181797,28-FEB-2000 US 60/185516, PR
              06-MAR-2000 US 60/187128
              PI Lawrence blatt,james mcswiggen,blatto m chorlila,peter pi
              harbali
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              Location/Qualifiers
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Query Match      54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGCGUGUUAAGCGU 22
Db 23 AGGTGCTGGTGAAGGCAT 6
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Qy      1  UGAGAGGGGCGUGG 13
Db      16 TGAGAGGGGCTGG 4

RESULT 11
BD379516/c
LOCUS
DEFINITION Method and Reagent for the Modulation and Diagnosis of CD20 and
ACCESSION BD379516
VERSION    BD379516.1 GI:92278609
KEYWORDS   JP 2003525037-A/740.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Blatt,L., Mcswiggen,J., Chorlila,B.M. and Harbali,P.
TITLE      Method and Reagent for the Modulation and Diagnosis of CD20 and
JOURNAL    NOGO Gene Expression
COMMENT     Patent: JP 2003525037-A 740 26-AUG-2003;
            Ribozyme Pharmaceuticals Inc
            OS Artificial Sequence
            PN JP 2003525037-A/740
            PD 26-AUG-2003
            PF 09-FEB-2001 JP 2001558241
            PR 11-FEB-2000 US 60/181797,28-FEB-2000 US 60/185516, PR
            PI Lawrence blatt,james mcswiggen,balatto m chorlila,peter PI
            harbali
CC Description of Artificial Sequence: Nucleic Acid FH Key
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Query Match 54.2%; Score 13; DB 2; Length 17;
Best Local Similarity 84.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db      14 TGAGAGGGGCTGG 2

RESULT 12
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LOCUS
DEFINITION Method and Reagent for the Modulation and Diagnosis of CD20 and
ACCESSION BD379517
VERSION    BD379517.1 GI:92278610
KEYWORDS   JP 2003525037-A/741.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Blatt,L., Mcswiggen,J., Chorlila,B.M. and Harbali,P.
TITLE      Method and Reagent for the Modulation and Diagnosis of CD20 and
JOURNAL    NOGO Gene Expression
COMMENT     Patent: JP 2003525037-A 741 26-AUG-2003;
            Ribozyme Pharmaceuticals Inc
            OS Artificial Sequence
            PN JP 2003525037-A/741
            PD 26-AUG-2003
            PF 09-FEB-2001 JP 2001558241
            PR 11-FEB-2000 US 60/181797,28-FEB-2000 US 60/185516, PR
            PI Lawrence blatt,james mcswiggen,balatto m chorlila,peter PI
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CC Description of Artificial Sequence: Nucleic Acid FH Key
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ORIGIN
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Best Local Similarity 84.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1  UGAGAGGGGCGUGG 13
Db      15 TGAGAGGGGCTGG 3

RESULT 13
BD379518/c
LOCUS
DEFINITION Method and Reagent for the Modulation and Diagnosis of CD20 and
ACCESSION BD379518
VERSION    BD379518.1 GI:92278611
KEYWORDS   JP 2003525037-A/742.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Blatt,L., Mcswiggen,J., Chorlila,B.M. and Harbali,P.
TITLE      Method and Reagent for the Modulation and Diagnosis of CD20 and
JOURNAL    NOGO Gene Expression
COMMENT     Patent: JP 2003525037-A 742 26-AUG-2003;
            Ribozyme Pharmaceuticals Inc
            OS Artificial Sequence
            PN JP 2003525037-A/742
            PD 26-AUG-2003
            PF 09-FEB-2001 JP 2001558241
            PR 11-FEB-2000 US 60/181797,28-FEB-2000 US 60/185516, PR
            PI Lawrence blatt,james mcswiggen,balatto m chorlila,peter PI
            harbali
CC Description of Artificial Sequence: Nucleic Acid FH Key
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Best Local Similarity 84.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1  UGAGAGGGGCGUGG 13
Db      13 TGAGAGGGGCTGG 1

RESULT 14
AX215297/c
LOCUS
DEFINITION Sequence 739 from Patent WO0159103.
ACCESSION AX215297
VERSION    AX215297.1 GI:15525340
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1

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AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression

JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

## FEATURES

Location/Qualifiers  
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## ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 17;  
Best Local Similarity 84.6%; Pred. No. 1.5e+06;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGAGGGGCGG 13

Db 16 TGAGAGGGGCTGG 4

## RESULT 15

AX215298/c

LOCUS AX215298 17 bp RNA linear PAT 07-SEP-2001

DEFINITION Sequence 740 from Patent WO0159103.

ACCESSION AX215298

VERSION AX215298.1 GI:15525341

## KEYWORDS

synthetic construct  
synthetic construct  
other sequences; artificial sequences.

## SOURCE

ORGANISM

REFERENCE

1

Blatt, L., McSwiggen, J. and Chowrira, B.M.

Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression

Patent: WO 0159103-A 740 16-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

McSwiggen, James (US) ; Chowrira, Bharat M. (US)

## FEATURES

Location/Qualifiers  
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## ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 17;

Best Local Similarity 84.6%; Pred. No. 1.5e+06;

Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGAGGGGCGG 13

Db 15 TGAGAGGGGCTGG 3

Search completed: June 19, 2007, 13:51:02

Job time : 1109 secs

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:28:50 ; Search time 246 Seconds  
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Title: US-10-604-726A-6034  
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16: Geneseqn2007s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	15.8	65.8	24	6	ABQ04715 Oligonuc1
4	15.8	65.8	24	6	ABQ00358 Oligonuc1
5	15.8	65.8	24	6	ABQ11043 Oligonuc1
6	15.8	65.8	25	6	ABQ12538 Oligonuc1
7	15.8	65.8	25	6	ABQ12579 Oligonuc1
8	14.6	60.8	24	6	AAL50117 Human CAB
9	14.4	60.0	21	9	ADA24254 Major all
10	14.2	59.2	20	14	ADZ97885 Human ant
11	14.2	59.2	21	11	ADJ13347 Human DNA
12	14.2	59.2	25	3	AAA61591 Human Tes
13	14	58.3	25	9	ACI82777 Human mic
14	13.8	57.5	17	8	ACD57816 HCV DNAsy
15	13.8	57.5	17	12	ADI83268 HCV DNAsy
16	13.8	57.5	22	2	AAT47817 PCR prime
17	13.8	57.5	22	2	AAX04299 Mouse neu

18	13.6	56.7	21	14	ACL41634	ACL41634 CACNALD s
19	13.6	56.7	21	14	ACL41632	ACL41632 CACNALD t
20	13.6	56.7	21	14	ACL43064	ACL43064 CACNALD s
21	13.6	56.7	23	15	AEJ80377	AEJ80377 cDNA B586
22	13.2	55.0	19	14	AEA25301	AEA25301 Anti-mycos
23	13.2	55.0	19	14	AEA25458	AEA25458 Anti-mycos
24	13.2	55.0	20	10	ABZ99113	ABZ99113 Human PDE
25	13.2	55.0	20	11	ABD32144	ABD32144 Human PDE
26	13.2	55.0	20	12	ADJ60998	ADJ60998 Oligonuc1
27	13.2	55.0	20	12	ADO46487	ADO46487 Human Oll
28	13.2	55.0	20	14	ADZ97886	ADZ97886 Human ant
29	13.2	55.0	20	14	AED42052	AED42052 Antisense
30	13.2	55.0	21	11	ADJ13385	ADJ13385 Human DNA
31	13.2	55.0	21	13	ADU43508	ADU43508 Knock-dow
32	13.2	55.0	25	5	AAP85432	AAP85432 PCR prime
33	13.2	55.0	25	9	ACK10389	ACK10389 Human mic
34	13.2	55.0	25	10	AAD64634	AAD64634 Rat tauri
35	13.2	55.0	25	12	ADO61007	ADO61007 Human deb
36	13.2	55.0	25	14	AEC90171	AEC90171 CYP2D6 ge
37	13	54.2	17	4	ABK00741	ABK00741 Human NOG
38	13	54.2	17	4	ABK00742	ABK00742 Human NOG
39	13	54.2	17	4	ABK00739	ABK00739 Human NOG
40	13	54.2	17	4	ABK00740	ABK00740 Human NOG
41	13	54.2	20	6	AAS97797	AAS97797 Murine SA
42	13	54.2	20	12	ADM16137	ADM16137 Murine SA
43	13	54.2	21	14	ACL43063	ACL43063 CACNALD t
44	13	54.2	21	14	ACL42274	ACL42274 CACNALD t
45	13	54.2	25	9	ACI36340	ACI36340 Human mic

## ALIGNMENTS

RESULT 1  
ABQ11002  
ID ABQ11002 standard; DNA; 24 BP.  
XX  
AC ABQ11002;  
XX  
DT 11-JUN-2002 (first entry)  
XX  
DE Oligonucleotide adapter/capture probe 10993.  
XX  
KW Oligonucleotide array; adapter sequence; probe; ss.  
XX  
OS Synthetic.  
XX  
FN WO200216649-A2.  
XX  
PD 28-FEB-2002.  
XX  
PP 27-AUG-2001; 2001WO-US026519.  
XX  
PR 25-AUG-2000; 2000US-0227948P.  
PR 29-AUG-2000; 2000US-0228854P.  
XX  
(ILLU-) ILLUMINA INC.  
XX  
Gunderson K;  
XX  
WPI; 2002-292068/33.  
XX

Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.  
Claim 1; Page 225; 261pp; English.  
The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ00010-ABQ13409).

CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid

SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 6; Length 24;  
Best Local Similarity 73.7%; Pred. No. 1.4e+03;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGGUAAGGC 20  
||||| :||:|||||  
Db 4 GAGAGGGCGTGGTTAAGGC 22

RESULT 2  
ABQ04674  
ID ABQ04674 standard; DNA; 24 BP.

XX AC ABQ04674;

XX DT 11-JUN-2002 (first entry)

XX DE Oligonucleotide adapter/capture probe 4665.

XX KW Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

XX PF 27-AUG-2001; 2001WO-US026519.

XX PR 25-AUG-2000; 2000US-0227948P.

XX PR 29-AUG-2000; 2000US-0228854P.

XX FA (ILLU-) ILLUMINA INC.

XX XX Gunderson K;

XX PI WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting a  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.

PS Claim 1; Page 147; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-  
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid

SQ Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 6; Length 24;  
Best Local Similarity 73.7%; Pred. No. 1.4e+03;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGGUAAGGC 20

Db 4 GAGAGGGCGTGGTTAAGGC 22

RESULT 3

ABQ04715/c  
ID ABQ04715 standard; DNA; 24 BP.

XX AC ABQ04715;

XX DT 11-JUN-2002 (first entry)

XX DE Oligonucleotide adapter/capture probe 4706.

XX KW Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

XX PF 27-AUG-2001; 2001WO-US026519.

XX PR 25-AUG-2000; 2000US-0227948P.

XX PR 29-AUG-2000; 2000US-0228854P.

XX PA (ILLU-) ILLUMINA INC.

XX PI Gunderson K;

XX DR WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting a  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.

PS Claim 1; Page 147; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-  
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid

SQ Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 6; Length 24;  
Best Local Similarity 73.7%; Pred. No. 1.4e+03;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGGUAAGGC 20

Db 21 GAGAGGGCGTGGTTAAGGC 3

RESULT 4

ABQ00358

ID ABQ00358 standard; DNA; 24 BP.

XX AC ABQ00358;

XX DT 11-JUN-2002 (first entry)

XX DE Oligonucleotide adapter/capture probe 349.

XX KW Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.

XX PN WO200216649-A2.

XX PD 28-FEB-2002.

PF 27-AUG-2001; 2001WO-US026519.  
XX  
PR 25-AUG-2000; 2000US-0227948P.  
PR 29-AUG-2000; 2000US-0228854P.  
XX  
XX (ILLU-) ILLUMINA INC.  
XX Gunderson K;  
XX WPI; 2002-292068/33.  
XX  
XX Array comprising adapter sequences useful for immobilizing or detecting a  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.  
XX  
XX Claim 1; Page 52; 261pp; English.  
XX  
XX The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-  
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid  
XX  
XX Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 65.8%; Score 15.8; DB 6; Length 24;  
Best Local Similarity 73.7%; Pred. No. 1.4e+03;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GAGAGGGCGUGUUAAGGC 20  
Db 4 GAGAGGCGTTGGTTAAGGC 22  
RESULT 5  
ABQ11043/c  
ID ABQ11043 standard; DNA; 24 BP.  
XX AC ABQ11043;  
XX  
XX 11-JUN-2002 (first entry)  
XX Oligonucleotide adapter/capture probe 11034.  
XX Oligonucleotide array; adapter sequence; probe; ss.  
XX Synthetic.  
XX OS  
XX WO200216649-A2.  
XX PD 28-FEB-2002.  
XX  
XX 27-AUG-2001; 2001WO-US026519.  
XX  
XX 25-AUG-2000; 2000US-0227948P.  
PR 29-AUG-2000; 2000US-0228854P.  
XX  
XX (ILLU-) ILLUMINA INC.  
XX Gunderson K;  
XX WPI; 2002-292068/33.  
XX  
XX Array comprising adapter sequences useful for immobilizing or detecting a  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.  
XX  
XX Claim 1; Page 225; 261pp; English.  
XX

CC The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-  
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid  
XX  
XX Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 65.8%; Score 15.8; DB 6; Length 24;  
Best Local Similarity 73.7%; Pred. No. 1.4e+03;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GAGAGGGCGUGUUAAGGC 20  
Db 21 GAGAGGCGTTGGTTAAGGC 3  
RESULT 6  
ABQ12538  
ID ABQ12538 standard; DNA; 25 BP.  
XX AC ABQ12538;  
XX  
XX 11-JUN-2002 (first entry)  
XX Oligonucleotide adapter/capture probe 12529.  
XX Oligonucleotide array; adapter sequence; probe; ss.  
XX Synthetic.  
XX OS  
XX WO200216649-A2.  
XX PD 28-FEB-2002.  
XX  
XX 27-AUG-2001; 2001WO-US026519.  
XX  
XX 25-AUG-2000; 2000US-0227948P.  
PR 29-AUG-2000; 2000US-0228854P.  
XX  
XX (ILLU-) ILLUMINA INC.  
XX Gunderson K;  
XX WPI; 2002-292068/33.  
XX  
XX Array comprising adapter sequences useful for immobilizing or detecting a  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.  
XX  
XX Claim 1; Page 244; 261pp; English.  
XX  
XX The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-  
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid  
XX  
XX Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 65.8%; Score 15.8; DB 6; Length 25;  
Best Local Similarity 73.7%; Pred. No. 1.4e+03;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GAGAGGGCGUGUUAAGGC 20

```

||||| | :||:|||||
5 GAGAGGCGTTGGTTAAGGC 23

Db
RESULT 7
ABQ12579/c
ID ABQ12579 standard; DNA; 25 BP.
XX
XX
AC ABQ12579;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 12570.
XX
XX Oligonucleotide array; adapter sequence; probe; ss.
XX
XX Synthetic.
XX
XX WO200216649-A2.
XX
XX 28-FEB-2002.
XX
XX 27-AUG-2001; 2001WO-US026519.
XX
XX 25-AUG-2000; 2000US-0227948P.
XX
XX 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
XX
XX Gunderson K;
XX
XX WPI; 2002-292068/33.
XX
XX Array comprising adapter sequences useful for immobilizing or detecting a
XX target nucleic acid sequence, has different addresses comprising
XX different specific capture probes.
XX
XX Claim 1; Page 244; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX and contacting the modified target nucleic acid with (I). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid
XX
XX Sequence 25 BP; 5 A; 10 C; 2 G; 8 T; 0 U; 0 Other;
XX
Query Match 65.8%; Score 15.8; DB 6; Length 25;
Best Local Similarity 73.7%; Pred. No. 1.4e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGCGCGUUAAGGC 20
||||| | :||:|||||
22 GAGAGGCGTTGGTTAAGGC 4

Db
RESULT 8
AAL50117/c
ID AAL50117 standard; DNA; 24 BP.
XX
XX AAL50117;
XX
XX 28-JAN-2003 (first entry)
XX
XX Human CAB55953-1 ligand binding domain PCR primer #2.
XX
XX Human; CAB55953.1; nuclear hormone receptor ligand binding domain; LBDG3;
XX cancer; autoimmune disorder; inflammation; PCR; antiseborrheic;
XX dermatological; anti-HIV; neuroprotective; nephrotropic; antianginal;
XX

tranquillizer; antiarrhythmic; antiarteriosclerotic; antiaesthetic;
immunosuppressive; virucide; fungicide; antibacterial; antiparasitic;
cardiant; antidepressant; antidiabetic; vasotropic; antiinflammatory;
nephrotropic; cytostatic; antilipemic; hypotensive; antiallergic;
antithyroid; anorectic; osteopathic; analgesic; antipsoriatic; vulnery;
cerebroprotective; haemostatic; thrombolytic; cardiovascular disorder;
neurological disorder; infection; primer; ss.
Homo sapiens.
WO200270557-A2.
12-SEP-2002.
05-MAR-2002; 2002WO-GB000937.
05-MAR-2001; 2001GB-00005402.
(INPH-) INPHARMATICA LTD.
Fagan RJ, Phelps CB, Phillips T, Pierron VN, Allen KE, Allen JM;
Potter SJ;
WPI; 2002-698731/75.
New CAB55953.1 or LBDG3 polypeptide, useful as a nuclear hormone receptor
ligand-binding domain, or for manufacturing of a medicament for
diagnosing or treating cell proliferative disorders or
autoimmune/inflammatory disorders.
Example 2; Page 64; 122pp; English.
The present invention relates to the protein and coding sequences of a
human nuclear hormone receptor ligand binding domain designated
CAB55953.1 or LBDG3. The sequences are useful in the treatment of cancer,
autoimmune/inflammatory disorders, including allergy, inflammatory bowel
disease, arthritis, psoriasis and respiratory tract inflammation, asthma
and organ transplant rejection, cardiovascular disorders, including
hypertension, oedema, angina, atherosclerosis, thrombosis, sepsis, shock,
refusion injury, heart arrhythmia, and ischaemia, neurological
disorders including central nervous system disease, Alzheimer's disease,
brain injury, stroke, amyotrophic lateral sclerosis, anxiety, depression
and pain, developmental disorders, metabolic disorders including diabetes
mellitus, osteoporosis, lipid metabolism disorders, hyperthyroidism,
hyperparathyroidism, hypercalcaemia, hypercholesterolaemia,
hyperlipidaemia and obesity, renal disorders including
glomerulonephritis, renovascular hypertension, dermatological disorders
including acne, eczema and wound healing, negative effects of aging, and
acquired immunodeficiency syndrome (AIDS), viral, bacterial, fungal, and
parasitic infections, and other pathological conditions, particularly
those in which nuclear hormone receptors are implicated. The present
sequence is a PCR primer used to isolate the coding sequence of the
invention
Sequence 24 BP; 7 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 60.8%; Score 14.6; DB 6; Length 24;
Best Local Similarity 61.9%; Pred. No. 5.1e+03;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 AGAGGGCGCGUUAAGCGCUC 23
||||| | :||:|||||
23 AGAGGGCGCTTATTAACTCGTC 3

Db
RESULT 9
ADA24254/c
ID ADA24254 standard; DNA; 21 BP.
XX
XX ADA24254;
XX
XX 20-NOV-2003 (first entry)
XX

```

DE Major allergenic storage protein FAGAG1 PCR primer FAG19 SEQ ID NO:7.  
 KW food testing; allergen; PCR primer; Fagopyrum esculentum;  
 KW major allergenic storage protein; FAGAG1; ss.  
 XX  
 OS Synthetic.  
 OS Fagopyrum esculentum.  
 XX  
 PN WO2003068964-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 XX 26-SEP-2002; 2002WO-JP009982.  
 PF  
 XX 15-FEB-2002; 2002JP-00038930.  
 XX  
 XX (NISS ) NISSHIN SEIFUN GROUP INC.  
 PA  
 XX Yamakawa H, Suzuki E, Miyatake K, Hayakawa K;  
 PI WPI; 2003-637145/60.  
 XX  
 DR PCR-based method for testing foods using specific primers designed from  
 PT genes of target substance, useful in detecting trace components or  
 PT identifying specific harmful allergens in (processed) foods.  
 XX  
 PS Disclosure; Page 10; 38pp; Japanese.  
 XX  
 CC The present invention describes a method for testing the presence or  
 CC absence of a specific substance in a food by performing PCR with primers  
 CC which are designed on the basis of data obtained from a part of a gene of  
 CC the specific substance. Also described: (1) a similar method for  
 CC detecting a trace component contained in a food, or for identifying a  
 CC harmful allergen specific to a consumer of such substance by performing a  
 CC PCR with primers which are designed on the basis of data obtained from a  
 CC part of a gene of the specific substance; (2) primers for PCR applicable  
 CC in food testing which are designed on the basis of data obtained from a  
 CC part of a gene of the specific substance; and (3) kits for determining  
 CC concentration of a specific substance in the food containing the primers.  
 CC The methods are useful for testing foods, which can be used in detecting  
 CC trace components or identifying specific harmful allergens in (processed)  
 CC foods, particularly applicable in food safety and management. The present  
 CC sequence represents a PCR primer for a Fagopyrum esculentum major  
 CC allergenic storage protein designated FAGAG1, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 60.0%; Score 14.4; DB 9; Length 21;  
 Best Local Similarity 68.8%; Pred. No. 6.2e+03;  
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 7 GGGGUGGUUAGGCGU 22  
 DB 17 GGGCTGGTATGCGT 2  
 RESULT 10  
 ADZ97885/c  
 ID ADZ97885 standard; DNA; 20 BP.  
 XX  
 AC ADZ97885;  
 XX  
 DT 28-JUL-2005 (first entry)  
 XX  
 DE Human antisense oligonucleotide SEQ ID NO:39.  
 XX  
 KW protein interaction; antisense oligonucleotide; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2005112118-A1.  
 XX

PD 26-MAY-2005.  
 XX  
 PF 20-OCT-2003; 2003US-00690276.  
 XX  
 PR 02-DEC-1999; 99US-0168377P.  
 PR 02-DEC-1999; 99US-0168379P.  
 PR 25-FEB-2000; 2000US-0185056P.  
 PR 01-DEC-2000; 2000US-00727384.  
 PR 14-DEC-2000; 2000US-0255063P.  
 PR 21-DEC-2000; 2000US-0256986P.  
 PR 04-JAN-2001; 2001US-0259571P.  
 PR 04-JAN-2001; 2001US-0259572P.  
 PR 15-MAR-2001; 2001US-0276179P.  
 PR 19-MAR-2001; 2001US-0277013P.  
 PR 23-JUL-2001; 2001US-0307233P.  
 PR 14-DEC-2001; 2001US-00014814.  
 PR 21-DEC-2001; 2001US-00024599.  
 PR 04-JAN-2002; 2002US-00035343.  
 PR 04-JAN-2002; 2002US-00035344.  
 PR 14-MAR-2002; 2002US-00099924.  
 PR 18-MAR-2002; 2002US-00100503.  
 XX  
 XX (MYRI-) MYRIAD GENETICS INC.  
 PA  
 XX Cimborra D, Heichman K, Bartel P, Mauck K, Bush A;  
 PI WPI; 2005-371623/38.  
 XX  
 DR Modulating, in a host cell, a protein-protein interaction between first  
 PT protein, PRAK, (MAPKAPK5) and second protein, ERK3, (extracellular signal  
 PT -regulated kinase 3) by administering modulating compound.  
 XX  
 PS Disclosure; SEQ ID NO 39; 296pp; English.  
 XX  
 CC The invention relates to a method for modulating, in a host cell, a  
 CC protein-protein interaction between a first protein which is PRAK (P38-  
 CC regulated/activated protein kinase or MAPKAPK5) and a second protein  
 CC which is ERK3 (extracellular signal-regulated kinase 3). The method  
 CC comprises administering to the cell a compound capable of modulating the  
 CC protein-protein interaction. The method is useful in modulating in a host  
 CC cell a protein-protein interaction between a first protein which is PRAK  
 CC and a second protein which is ERK3 for treating inflammation or  
 CC inflammatory disorders, e.g., asthma, rheumatoid arthritis, juvenile  
 CC chronic arthritis, myositis, Crohn's disease, gastritis, colitis,  
 CC ulcerative colitis, inflammatory bowel disease, proctitis, pelvic  
 CC inflammatory disease, systemic lupus erythematosus, rhinitis,  
 CC conjunctivitis, scleritis, chronic inflammatory polyneuropathy, Tertiary  
 CC Lyme disease, psoriasis, dermatitis or eczema. In the exemplification of  
 CC the present invention examples of antisense oligonucleotides specific to  
 CC nucleic acids encoding individual proteins in tables 1 to 82 are provided  
 CC in SEQ ID NOS:11-223 (ADZ97857-ADZ98069).  
 XX  
 SQ Sequence 20 BP; 4 A; 10 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 59.2%; Score 14.2; DB 14; Length 20;  
 Best Local Similarity 68.4%; Pred. No. 7.7e+03;  
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 AGGGGUGGUUAGGCGUC 23  
 DB 20 AGGGCTGGTAAATGGAGTC 2  
 RESULT 11  
 ADJ13347/c  
 ID ADJ13347 standard; DNA; 21 BP.  
 XX  
 AC ADJ13347;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human DNA probe used to immobilise CpG methylated DNA seqID 474.  
 XX



KW probe; ss; chemical modification; methylation; array; CpG island;  
 KW tumour suppressor; p16; human; H69; H1618.

XX Homo sapiens.

XX US2003152950-A1.

XX 14-AUG-2003.

XX 27-JUN-2002; 2002US-00184085.

XX 27-JUN-2001; 2001US-0301370P.

XX (GARN/) GARNER H R.

XX (MINN/) MINNA J D.

XX (LUEB/) LUEBKE K J.

XX (BALO/) BALOG R P.

XX Garner HR, Minna JD, Luebke KJ, Balog RP;

XX WPI; 2003-874843/81.

XX Analysis of chemical modification of DNA involves obtaining sample of DNA

XX to be analyzed, treating DNA with chemical reagents that result in

XX different base sequences, and determining sequence of resulting DNA.

XX Example 1; SEQ ID NO 474; 210pp; English.

XX This invention relates to a novel method for analysing chemically

XX modified macromolecules. Specifically, it refers to a high throughput

XX method for the parallel analysis of many potential sites of chemical

XX modification (e.g. methylation) in DNA. The present invention describes

XX treating the DNA with one or more chemical reagents that result in

XX different base sequences depending upon the presence or absence of the

XX modification of interest. Accordingly, a device comprising an array of

XX probes is provided to hybridise with and select the altered DNA sequences

XX that comprise the modifications of interest such as a CpG island. In

XX particular, this invention refers to analysing the methylation pattern of

XX a region of the promoter for the tumour suppressor gene p16 from two

XX human lung tumour cell lines H69 and H1618. This oligonucleotide sequence

XX is a human DNA probe used to immobilise CpG methylated DNA of the

XX invention.

XX Sequence 21 BP; 6 A; 11 C; 1 G; 3 T; 0 U; 0 Other;

XX Query Match 59.2%; Score 14.2; DB 11; Length 21;

XX Best Local Similarity 63.2%; Pred. No. 7.7e+03;

XX Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

XX QY 1 UGAGAGGGCGUGUUAAGG 19

XX Db 20 TGAGGGGTGCTGTGAGG 2

XX RESULT 12

XX AAAA61591

XX ID AAA61591 standard; DNA; 25 BP.

KW probe; ss; chemical modification; methylation; array; CpG island;  
 KW tumour suppressor; p16; human; H69; H1618.

XX Homo sapiens.

XX US2003152950-A1.

XX 14-AUG-2003.

XX 27-JUN-2002; 2002US-00184085.

XX 27-JUN-2001; 2001US-0301370P.

XX (GARN/) GARNER H R.

XX (MINN/) MINNA J D.

XX (LUEB/) LUEBKE K J.

XX (BALO/) BALOG R P.

XX Garner HR, Minna JD, Luebke KJ, Balog RP;

XX WPI; 2003-874843/81.

XX Analysis of chemical modification of DNA involves obtaining sample of DNA

XX to be analyzed, treating DNA with chemical reagents that result in

XX different base sequences, and determining sequence of resulting DNA.

XX Example 1; SEQ ID NO 474; 210pp; English.

XX This invention relates to a novel method for analysing chemically

XX modified macromolecules. Specifically, it refers to a high throughput

XX method for the parallel analysis of many potential sites of chemical

XX modification (e.g. methylation) in DNA. The present invention describes

XX treating the DNA with one or more chemical reagents that result in

XX different base sequences depending upon the presence or absence of the

XX modification of interest. Accordingly, a device comprising an array of

XX probes is provided to hybridise with and select the altered DNA sequences

XX that comprise the modifications of interest such as a CpG island. In

XX particular, this invention refers to analysing the methylation pattern of

XX a region of the promoter for the tumour suppressor gene p16 from two

XX human lung tumour cell lines H69 and H1618. This oligonucleotide sequence

XX is a human DNA probe used to immobilise CpG methylated DNA of the

XX invention.

XX Sequence 21 BP; 6 A; 11 C; 1 G; 3 T; 0 U; 0 Other;

XX Query Match 59.2%; Score 14.2; DB 11; Length 21;

XX Best Local Similarity 63.2%; Pred. No. 7.7e+03;

XX Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

XX QY 1 UGAGAGGGCGUGUUAAGG 19

XX Db 20 TGAGGGGTGCTGTGAGG 2

XX RESULT 12

XX AAAA61591

XX ID AAA61591 standard; DNA; 25 BP.

PD 11-MAY-2000.

XX 02-NOV-1999; 99WO-JP006111.

XX 04-NOV-1998; 98JP-00313366.

XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Senoo C, Numata M;

XX WPI; 2000-365604/31.

XX Trypsin family serine proteases expressed specifically in mature testis  
 for development of methods for diagnosis and treatment of sterility and  
 for contraception.

XX Example 9; Page 45; 121pp; Japanese.

XX The invention relates to novel murine and human testis specific serine  
 proteases (Tespec PRO; AAB03156-B03160) and to cDNAs encoding them  
 (AAA61558-A61562). It also encompasses expression vectors and host cells  
 comprising a nucleotide sequence encoding a protease of the invention,

XX inhibitors of the proteases and antibodies against the proteases. The  
 novel proteases are members of the trypsin family of serine proteases,  
 having the serine and histidine active site signatures characteristic of  
 this family. The proteases are specifically expressed in mature testis  
 and participate in the differentiation and maturation of sperm. The  
 proteases are potentially useful for the development of pharmaceuticals  
 for the treatment of male infertility and other male reproductive  
 disorders, and for the development of contraceptives. They may also be  
 used as reagents for the diagnosis of male infertility. Sequences  
 AAA61590-A61593 represent RACE (rapid amplification of cDNA ends) PCR  
 primers used in the isolation of cDNA encoding human Tespec PRO-3  
 (AAA61561)

XX Sequence 25 BP; 4 A; 2 C; 10 G; 9 T; 0 U; 0 Other;

XX Query Match 59.2%; Score 14.2; DB 3; Length 25;

XX Best Local Similarity 63.2%; Pred. No. 7.9e+03;

XX Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

XX QY 4 GAGGGCGUGUUAAGCGU 22

XX Db 3 GATGGGCTAGTTAAGTCGT 21

XX RESULT 13

XX ACI82777

XX ID ACI82777 standard; DNA; 25 BP.

XX ACI82777;

XX 14-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 82768.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 genetic variation; biallelic marker; polymorphism; human;  
 cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.  
XX New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX Claim 1; SEQ ID NO 82768; 9pp; English.  
XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying allelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX SQ Sequence 25 BP; 6 A; 4 C; 10 G; 5 T; 0 U; 0 Other;  
Query Match 58.3%; Score 14; DB 9; Length 25;  
Best Local Similarity 59.1%; Pred. No. 9.8e+03;  
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 2 GACAGGGGCGUGUUAAGCGUC 23  
Db 1 GACAGGGGATCGTTAGACGTC 22  
RESULT 14  
ACD57816/c  
ID ACD57816 standard; RNA; 17 BP.  
XX ACD57816;  
XX 23-SEP-2003 (first entry)  
XX HCV DNzyme substrate sequence #514.  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX Hepatitis C virus.  
XX WO200281494-A1.  
XX 17-OCT-2002.  
XX 26-MAR-2002; 2002WO-US0009187.  
XX 26-MAR-2001; 2001US-00817879.  
XX 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX Claim 1; Page 243; 387pp; English.  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNzyme or minus strand DNzyme sequences disclosed in the present  
CC invention  
XX SQ Sequence 17 BP; 4 A; 9 C; 1 G; 0 T; 3 U; 0 Other;  
Query Match 57.5%; Score 13.8; DB 8; Length 17;  
Best Local Similarity 70.6%; Pred. No. 1.2e+04;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 6 GGGGCGUGUUAAGCGGU 22  
Db 17 GGGGCGAGTTAAGTGT 1  
RESULT 15  
ADI83268/c  
ID ADI83268 standard; RNA; 17 BP.  
XX ADI83268;  
XX 22-SEP-2005 (revised)  
XX 03-JUN-2004 (first entry)  
XX HCV DNzyme substrate sequence #514.  
XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
KW HCV infection; type I interferon; DNzyme.  
XX Hepatitis C virus.  
XX OS Hepatitis C virus.  
XX PN US2003125270-A1.  
XX XX

PD 03-JUL-2003.  
 XX  
 PF 18-DEC-2000; 2000US-00740332.  
 XX  
 PR 18-DEC-2000; 2000US-00740332.  
 XX  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (ROBE/) ROBERTS E.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;  
 XX  
 DR WPI; 2004-031273/03.  
 XX  
 XX Enzymatic nucleic acid molecules which specifically cleave RNA derived  
 PT from Hepatitis C virus (HCV), useful for the treatment of HCV infections,  
 PT especially in combination with type I interferon therapy.  
 XX  
 PS Claim 1; SEQ ID NO 514; 198pp; English.  
 XX  
 CC The invention relates to an enzymatic nucleic acid molecule which  
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which  
 CC the binding arms of the enzymatic nucleic acid molecule comprises  
 CC sequences complementary to any of the defined substrate sequences given  
 CC in the specification. The nucleic acid molecule may be administered for  
 CC the treatment of HCV infections, especially in combination with type I  
 CC interferons. The present sequence represents a HCV DNazyme substrate  
 CC sequence.  
 CC  
 CC Revised record issued on 22-SEP-2005 : No correction was made to this  
 CC record  
 XX  
 SQ Sequence 17 BP; 4 A; 9 C; 1 G; 0 T; 3 U; 0 Other;  
  
 Query Match 57.5%; Score 13.8; DB 12; Length 17;  
 Best Local Similarity 70.6%; Pred. No. 1.2e+04;  
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
 Qy 6 GGGCGUGGUUAGGCGU 22  
 Db 17 GGGCAGGTTAAGGTGT 1  
  
 Search completed: June 19, 2007, 13:01:30  
 Job time : 249.5 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C 1	14	58.3	25	3	US-09-396-196G-15707	Sequence 15707, A
C 2	13.8	57.5	22	2	US-08-179-738-12	Sequence 12, Appl
C 3	13.8	57.5	22	2	US-08-628-145-12	Sequence 23, Appl
C 4	13.2	55.0	25	2	US-08-295-814E-23	Sequence 23, Appl
C 5	13.2	55.0	25	3	US-09-343-361-23	Sequence 23, Appl
C 6	12.8	53.3	19	2	US-08-460-751-27	Sequence 27, Appl
C 7	12.8	53.3	25	3	US-09-641-259B-31	Sequence 31, Appl
C 8	12.6	52.5	19	3	US-10-059-579A-123	Sequence 123, App
C 9	12.6	52.5	20	3	US-09-166-186-119	Sequence 119, App
C 10	12.6	52.5	20	3	US-09-313-932-119	Sequence 119, App
C 11	12.6	52.5	20	3	US-09-980-052-51	Sequence 51, Appl
C 12	12.6	52.5	21	3	US-08-520-373D-31	Sequence 31, Appl
C 13	12.6	52.5	25	3	US-09-443-067-45	Sequence 45, Appl
C 14	12.6	52.5	25	3	US-09-396-196G-3644	Sequence 3644, Ap
C 15	12.6	52.5	25	3	US-09-396-196G-29254	Sequence 29254, A
C 16	12.4	51.7	24	3	US-09-630-377-11	Sequence 11, Appl
C 17	12.4	51.7	25	3	US-09-396-196G-41852	Sequence 41852, A
C 18	12.4	51.7	25	3	US-09-396-196G-58488	Sequence 58488, A
C 19	12.4	51.7	25	3	US-09-396-196G-73489	Sequence 73489, A
C 20	12.4	51.7	25	3	US-09-396-196G-78586	Sequence 78586, A
C 21	12.4	51.7	25	3	US-09-396-196G-122139	Sequence 122139,
C 22	12.4	51.7	25	3	US-09-396-196G-122140	Sequence 122140,
C 23	12.2	50.8	19	3	US-09-422-978-9132	Sequence 9132, Ap

STATE: California  
COUNTRY: U.S.A  
ZIP: 94301  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/179,738  
FILING DATE: 10-JAN-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Robins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5998-0017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-179-738-12

Query Match 57.5%; Score 13.8; DB 2; Length 22;  
Best Local Similarity 70.6%; Pred. No. 2.5e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAGGGCUGGUUAGG 19  
|||||:|:|:|  
DB 17 AGAGGAGCTGTTTCAGG 1

RESULT 3  
US-08-628-145-12/c  
; Sequence 12, Application US/08628145  
; Patent No. 5872214  
; GENERAL INFORMATION:  
; APPLICANT: Seizinger, Bernd R.  
; APPLICANT: Kley, Nikolai A.  
; APPLICANT: Bianchi, Albert B.  
; TITLE OF INVENTION: No. 5872214el NF2 Isoforms  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reed & Robins  
; STREET: 635 Bryant Street  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: U.S.A  
; ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/628,145  
FILING DATE: 04-APR-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/179,738  
FILING DATE: 10-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Robins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5998-0017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-628-145-12

Query Match 57.5%; Score 13.8; DB 2; Length 22;  
Best Local Similarity 70.6%; Pred. No. 2.5e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAGGGCUGGUUAGG 19  
|||||:|:|:|  
DB 17 AGAGGAGCTGTTTCAGG 1

RESULT 4  
US-08-295-814E-23/c  
; Sequence 23, Application US/08295814E  
; Patent No. 5658786  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Kelli E.  
; APPLICANT: Borden, Laurence A.  
; APPLICANT: Hartig, Paul R.  
; APPLICANT: Weinsank, Richard L.  
; TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA  
; TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,814E  
FILING DATE: DECEMBER 19, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: White, John  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 40558-B-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-295-814E-23

Query Match 55.0%; Score 13.2; DB 2; Length 25;  
Best Local Similarity 66.7%; Pred. No. 4.9e+03;  
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGGGCUGGUUAGGCGU 22  
|||||:|:|:|  
DB 23 AGGTGCTGCTGAGGCAT 6

RESULT 5  
US-09-343-361-23/c

; Sequence 23, Application US/09343361  
; Patent No. 6225115  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Kelli E. et al  
; TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses  
; FILE REFERENCE: 40558-D  
; CURRENT APPLICATION NUMBER: US/09/343,361  
; CURRENT FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO 23  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-343-361-23

Query Match 55.0%; Score 13.2; DB 3; Length 25;  
Best Local Similarity 66.7%; Pred. No. 4.9e+03;  
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGUAGGCGU 22  
Db 23 AGGTGCTGGTGAAGGCAT 6

RESULT 6  
US-08-460-751-27  
; Sequence 27, Application US/08460751  
; Patent No. 5891628  
; GENERAL INFORMATION:  
; APPLICANT: Reeders, Stephen  
; APPLICANT: Schneider, Michael  
; APPLICANT: Glucksmann, Sandra  
; TITLE OF INVENTION: IDENTIFICATION OF POLYCYSTIC KIDNEY  
; TITLE OF INVENTION: DISEASE GENE, DIAGNOSTICS AND TREATMENT  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,751  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/413,580  
; FILING DATE: 03-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7638-005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA

US-08-460-751-27

Query Match 53.3%; Score 12.8; DB 2; Length 19;  
Best Local Similarity 62.5%; Pred. No. 7.3e+03;  
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 9 GCUGGUUAGGCGUCC 24  
Db 1 GCTCTTTAAGGCGTCC 16

RESULT 7  
US-09-641-259B-31/C  
; Sequence 31, Application US/09641259B  
; Patent No. 6468756  
; GENERAL INFORMATION:  
; APPLICANT: Bonini, James A  
; APPLICANT: Borowsky, Beth E  
; APPLICANT: Adham, Nika  
; APPLICANT: Boyle, No. 64687561  
; APPLICANT: Thompson, Thelma O.  
; TITLE OF INVENTION: DNA Encoding SNORF25 Receptor  
; FILE REFERENCE: 1795/56095-B/JPW/ADM  
; CURRENT APPLICATION NUMBER: US/09/641,259B  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: PCT/US00/04413  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 09/387,699  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: US 09/255,376  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer/ Probe  
US-09-641-259B-31

Query Match 53.3%; Score 12.8; DB 3; Length 25;  
Best Local Similarity 68.8%; Pred. No. 7.6e+03;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGGCGUGUUAAGG 19  
Db 20 GAGGGCGTGTAAATG 5

RESULT 8  
US-10-059-579A-123/C  
; Sequence 123, Application US/10059579A  
; Patent No. 6835541  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: SUKUMAR, Saraswati  
; APPLICANT: EVRON, Ella  
; APPLICANT: DOOLEY, William C.  
; APPLICANT: DAVIDSON, Nancy  
; APPLICANT: FACKLER, Mary Jo.  
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY  
; FILE REFERENCE: JHU1630-1  
; CURRENT APPLICATION NUMBER: US/10/059,579A  
; CURRENT FILING DATE: 2002-01-28  
; PRIOR APPLICATION NUMBER: US 09/771,357  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 123  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial sequence



```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PRIMER
; OTHER INFORMATION: PRIMER 1
US-08-520-373D-31

Query Match      52.5%; Score 12.6; DB 3; Length 21;
Best Local Similarity 63.2%; Pred. No. 9.2e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      3 AGAGGGGCGUUAAGGCG 21
Db      19 ATAAAGGCTGTTAAGGTG 1

RESULT 13
US-09-443-067-45
; Sequence 45, Application US/09443067
; Patent No. 6627794
; GENERAL INFORMATION:
; APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
; APPLICANT: ORGANISATION
; TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
; TITLE OF INVENTION: pineapple
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,067
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: US 08/976, 222
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: PCT/AU98/00362
; EARLIER FILING DATE: 1998-05-19
; EARLIER APPLICATION NUMBER: AU PP3898
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: AU PP6849
; EARLIER FILING DATE: 1997-05-19
; EARLIER APPLICATION NUMBER: AU PP5600
; EARLIER FILING DATE: 1995-09-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-443-067-45

Query Match      52.5%; Score 12.6; DB 3; Length 25;
Best Local Similarity 63.2%; Pred. No. 9.5e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      5 AGGGGCGUUAAGGCGUC 23
Db      6 ATGGGATGCTGAAGGTGTC 24

RESULT 14
US-09-396-196G-3644/c
; Sequence 3644, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
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; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3644
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-3644

Query Match      52.5%; Score 12.6; DB 3; Length 25;
Best Local Similarity 68.4%; Pred. No. 9.5e+03;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      3 AGAGGGGCGUUAAGGCG 21
Db      21 AGAGAGTCTGGTGAAGACG 3

RESULT 15
US-09-396-196G-29254
; Sequence 29254, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29254
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-29254

Query Match      52.5%; Score 12.6; DB 3; Length 25;
Best Local Similarity 57.9%; Pred. No. 9.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 UGAGAGGGGCGUUAAGG 19
Db      7 TCAGAGGCGCTAGTTAATG 25

Search completed: June 19, 2007, 13:10:06
Job time : 256.5 secs
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GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:01:01 ; Search time 1262 Seconds  
(without alignments)  
233.679 Million cell updates/sec

Title: US-10-604-726a-6034

Perfect score: 24  
Sequence: 1 usagagggcugguuagcgucc 24

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 22906428

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:

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- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
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- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.6	69.2	25	13	US-11-036-317-713202
C 2	16.2	67.5	25	9	US-10-719-900-888593
C 3	15.8	65.8	24	3	US-09-940-185-365
C 4	15.8	65.8	25	3	US-09-940-185-4341
C 5	15.8	65.8	25	13	US-11-036-317-751276
C 6	15.6	65.0	25	13	US-11-036-317-508584
C 7	15.6	65.0	25	13	US-11-036-317-648052
C 8	15.2	63.3	21	11	US-10-310-914A-310484
C 9	15.2	63.3	21	11	US-10-310-914A-310485
C 10	15.2	63.3	21	11	US-10-310-914A-310486
C 11	15.2	63.3	21	11	US-10-310-914A-310487
C 12	15.2	63.3	21	11	US-10-310-914A-594029
C 13	15.2	63.3	21	11	US-10-310-914A-1286104
C 14	15.2	63.3	22	11	US-10-310-914A-1056699
C 15	15.2	63.3	22	11	US-10-310-914A-594065
C 16	15.2	63.3	24	11	US-10-310-914A-1286102
C 17	15.2	63.3	25	9	US-10-719-900-623329

18	15.2	63.3	25	15	US-11-121-849-463132	Sequence 463132,
C 19	15	62.5	25	9	US-10-719-900-470368	Sequence 470368,
20	15	62.5	25	9	US-10-719-900-473457	Sequence 473457,
21	15	62.5	25	13	US-11-036-317-537085	Sequence 537085,
C 22	15	62.5	25	13	US-11-036-317-657262	Sequence 657262,
C 23	15	62.5	25	13	US-11-036-317-713203	Sequence 713203,
C 24	15	62.5	25	13	US-11-036-317-798014	Sequence 798014,
C 25	14.8	61.7	21	11	US-10-310-914A-752575	Sequence 752575,
C 26	14.6	61.7	22	11	US-10-310-914A-175870	Sequence 175870,
C 27	14.6	60.8	21	11	US-10-310-914A-371120	Sequence 371120,
28	14.6	60.8	23	11	US-10-310-914A-707100	Sequence 707100,
C 29	14.6	60.8	23	11	US-10-310-914A-1006052	Sequence 1006052,
C 30	14.6	60.8	24	9	US-10-469-866-23	Sequence 23, Appl
31	14.6	60.8	24	11	US-10-310-914A-224322	Sequence 224322,
32	14.6	60.8	25	8	US-10-719-956-115625	Sequence 115625,
33	14.6	60.8	25	8	US-10-719-956-115627	Sequence 115627,
C 34	14.6	60.8	25	9	US-10-719-900-888594	Sequence 888594,
C 35	14.6	60.8	25	13	US-11-036-317-892224	Sequence 892224,
C 36	14.6	60.8	25	13	US-11-036-317-966783	Sequence 966783,
37	14.6	60.8	25	13	US-11-121-849-363	Sequence 363, App
C 38	14.4	60.0	21	12	US-10-504-589A-7	Sequence 7, Appli
C 39	14.4	60.0	24	11	US-10-310-914A-1339473	Sequence 1339473,
40	14.4	60.0	25	8	US-10-719-956-605791	Sequence 605791,
41	14.4	60.0	25	8	US-10-719-956-605792	Sequence 605792,
42	14.4	60.0	25	13	US-11-036-317-213436	Sequence 213436,
43	14.4	60.0	25	13	US-11-036-317-884459	Sequence 884459,
C 44	14.2	59.2	19	11	US-10-310-914A-1056695	Sequence 1056695,
45	14.2	59.2	19	14	US-11-083-784-1176587	Sequence 1176587,

#### ALIGNMENTS

##### RESULT 1

US-11-036-317-713202/c

; Sequence 713202, Application US/11036317

; Publication No. US20050214823A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036.317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 713202

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-713202

Query Match	69.2%	Score 16.6;	DB 13;	Length 25;
Best Local Similarity	65.2%	Pred. No. 8.8e+02;		
Matches	15;	Conservative	4;	Mismatches
			4;	Indels
				Gaps
				0;

##### RESULT 2

US-10-719-900-888593/c

; Sequence 888593, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

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; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 888593
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-888593

Query Match      67.5%; Score 16.2; DB 9; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAGGGGCGUGUUAAGGCGUCC 24
    |||||:|:|||||:|:|
DB 23 GAGGGCTAGTTAAGGCTTCC 3

RESULT 3
US-09-940-185-365
; Sequence 365, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 365
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-365

Query Match      65.8%; Score 15.8; DB 3; Length 24;
Best Local Similarity 73.7%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGUUAAGGC 20
DB 4 GAGAGGCGTTGGTTAAGGC 22

RESULT 4
US-09-940-185-4341
; Sequence 4341, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4341
; LENGTH: 25
; TYPE: DNA

```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4341

Query Match      65.8%; Score 15.8; DB 3; Length 25;
Best Local Similarity 73.7%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGCGUGUUAAGGC 20
    |||||:|:|||||:|:|
DB 5 GAGAGGCGTTGGTTAAGGC 23

RESULT 5
US-11-036-317-751276/c
; Sequence 751276, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 751276
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-751276

Query Match      65.8%; Score 15.8; DB 13; Length 25;
Best Local Similarity 68.4%; Pred. No. 2.1e+03;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 UGAGAGGGCGUGUUAAGG 19
    :|:|||||:|:|:|
DB 25 TCAAAGGGCGCTGGTTAAGG 7

RESULT 6
US-11-036-317-508584/c
; Sequence 508584, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 508584
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-508584

Query Match      65.0%; Score 15.6; DB 13; Length 25;
Best Local Similarity 63.6%; Pred. No. 2.6e+03;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 AGAGGGCGUGUUAAGGCGUCC 24
    |||||:|:|||||:|:|
DB 25 AGAGGGCGCTGGTTAAGGTC 4

```

```
RESULT 7
US-11-036-317-648052/c
; Sequence 648052, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 648052
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-648052

Query Match      65.0%; Score 15.6; DB 13; Length 25;
Best Local Similarity 63.6%; Pred. No. 2.6e+03;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      2 GAGAGGGCGGCUUUAAGGCGUC 23
      ||||| |::: ||| |::|
Db      22 GAGAGGCCCTGTTCAAGGAGTC 1

RESULT 8
US-10-310-914A-310484/c
; Sequence 310484, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310484
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310484

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 UGAGAGGGCGGCUUUAAGGC 20
      :||||| |::: ||| |::|
Db      21 TGAGAGGGGAAGGCTAAGGC 2

RESULT 9
US-10-310-914A-310485/c
; Sequence 310485, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310485
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310485

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 UGAGAGGGCGGCUUUAAGGC 20
      :||||| |::: ||| |::|
Db      21 TGAGAGGGGAAGGCTAAGGC 2

RESULT 10
US-10-310-914A-310486/c
; Sequence 310486, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310486
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310486

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 UGAGAGGGCGGCUUUAAGGC 20
      :||||| |::: ||| |::|
Db      21 TGAGAGGGGAAGGCTAAGGC 2

RESULT 11
US-10-310-914A-310487/c
; Sequence 310487, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 310487
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310487

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 UGAGAGGGCGGCUUUAAGGC 20
      :||||| |::: ||| |::|
Db      21 TGAGAGGGGAAGGCTAAGGC 2
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```
RESULT 12
US-10-310-914A-594029
; Sequence 594029, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 594029
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-594029

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GAGAGGGCGUGGUUAAAGCG 21
      |||||:|||||
Db      2 GAGAGGGCGUGGUUAGGCG 21

RESULT 13
US-10-310-914A-1286104/c
; Sequence 1286104, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1286104
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1286104

Query Match      63.3%; Score 15.2; DB 11; Length 21;
Best Local Similarity 80.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GAGAGGGCGUGGUUAAAGCG 21
      |||||:|||||
Db      2 GAGAGGGCGUGGUUAGGCG 21

RESULT 14
US-10-310-914A-1056699/c
; Sequence 1056699, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 1056699
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1056699

Query Match      63.3%; Score 15.2; DB 11; Length 22;
Best Local Similarity 80.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GAGAGGGCGUGGUUAAAGCG 21
      |||||:|||||
Db      21 GAGAGGGCGUGGUUAGGCG 2

RESULT 15
US-10-310-914A-594065
; Sequence 594065, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 594065
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-594065

Query Match      63.3%; Score 15.2; DB 11; Length 24;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GAGAGGGCGUGGUUAAAGCG 21
      |||||:|||||
Db      4 GAGAGGGCGUGGUUAGGCG 23

Search completed: June 19, 2007, 16:27:48
Job time : 1263 secs
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GenCore version 6.2.1  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 13:01:51 ; Search time 610 Seconds  
(without alignments)  
405.912 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24  
Sequence: 1 uGAGAGGGGCGUUAAGCGUCC 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 15754707 seqs, 5162687648 residues

Total number of hits satisfying chosen parameters: 17957554

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.2	63.3	25	11	US-10-956-160-156795
2	15.2	63.3	25	11	US-10-956-160-157603
3	14.8	61.7	25	11	US-10-956-160-123988
C 4	14.4	60.0	17	9	US-10-709-691B-1378586
5	14.2	59.2	19	10	US-10-714-333A-1176587
6	14.2	59.2	19	17	US-11-093-832-1176587
C 7	14	58.3	22	9	US-10-709-691B-19539
C 8	14	58.3	22	9	US-10-709-691B-101448
C 9	14	58.3	22	9	US-10-709-691B-123481
C 10	14	58.3	22	9	US-10-709-691B-134127
C 11	14	58.3	22	9	US-10-709-691B-142124

C 12	14	58.3	22	9	US-10-709-691B-145999
C 13	14	58.3	22	9	US-10-709-691B-153005
C 14	14	58.3	22	9	US-10-709-691B-187400
C 15	14	58.3	22	9	US-10-709-691B-197873
C 16	14	58.3	22	9	US-10-709-691B-208809
C 17	14	58.3	22	9	US-10-709-691B-248124
C 18	13.8	57.5	19	10	US-10-714-333A-494904
C 19	13.8	57.5	19	17	US-11-093-832-494904
C 20	13.8	57.5	22	9	US-10-709-691B-42828
C 21	13.8	57.5	22	9	US-10-709-691B-225295
C 22	13.8	57.5	25	9	US-10-859-198-254645
C 23	13.8	57.5	25	14	US-11-217-529-40910
C 24	13.6	56.7	21	13	US-11-509-413-2704
C 25	13.6	56.7	21	13	US-11-509-413-4136
C 26	13.6	56.7	21	13	US-11-130-645A-11011
C 27	13.6	56.7	22	19	US-10-709-691B-1899145
C 28	13.4	55.8	18	8	US-10-709-691B-1969471
C 29	13.4	55.8	18	8	US-10-709-691B-1890291
C 30	13.4	55.8	19	8	US-10-709-691B-1890632
C 31	13.4	55.8	19	8	US-10-709-691B-1899146
C 32	13.4	55.8	19	8	US-10-709-691B-1956798
C 33	13.4	55.8	19	8	US-10-709-691B-1962777
C 34	13.4	55.8	19	8	US-10-709-691B-1969470
C 35	13.4	55.8	19	8	US-10-709-691B-2612611
C 36	13.4	55.8	19	8	US-10-709-691B-578997
C 37	13.4	55.8	19	9	US-10-714-333A-1365090
C 38	13.4	55.8	19	11	US-10-714-333A-46028
C 39	13.4	55.8	19	11	US-10-714-333A-46048
C 40	13.4	55.8	19	17	US-11-093-832-46028
C 41	13.4	55.8	19	17	US-11-093-832-46048
C 42	13.4	55.8	19	17	US-11-093-832-1365090
C 43	13.4	55.8	20	8	US-10-709-691B-1892935
C 44	13.4	55.8	20	8	US-10-709-691B-1893092
C 45	13.4	55.8	20	8	US-10-709-691B-1893092

#### ALIGNMENTS

RESULT 1  
US-10-956-160-156795  
; Sequence 156795, Application US/10956160  
; Publication No. US20070009899A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL  
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES  
; FILE REFERENCE: 031896-044000 (AM101084)  
; CURRENT APPLICATION NUMBER: US/10/956.160  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 222274  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 156795  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-956-160-156795

Query Match 63.3%; Score 15.2; DB 11; Length 25;  
Best Local Similarity 70.0%; Pred. No. 4.9e+03;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 4 GAGGGCGGUGUUAAGCGUCC 23  
|||||:|:|||||  
Db 5 GAGGGACTGCTTAAGCGCAC 24  
  
RESULT 2  
US-10-956-160-157603  
; Sequence 157603, Application US/10956160  
; Publication No. US20070009899A1  
; GENERAL INFORMATION:

APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL  
TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES  
FILE REFERENCE: 031896-044000 (AM101084)  
CURRENT APPLICATION NUMBER: US/10/956,160  
CURRENT FILING DATE: 2004-10-04  
NUMBER OF SEQ ID NOS: 222274  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 157603  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-10-956-160-157603

Query Match 63.3%; Score 15.2; DB 11; Length 25;  
Best Local Similarity 70.0%; Pred. No. 4.9e+03;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAGGGCGUGGUUAGGCGUC 23  
|||||:|:|:|:|:|:|  
Db 2 GAGGACTGCTTAAGCGAC 21

RESULT 3  
US-10-956-160-123988  
Sequence 123988, Application US/10956160  
Publication No. US20070009899A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL  
TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES  
FILE REFERENCE: 031896-044000 (AM101084)  
CURRENT APPLICATION NUMBER: US/10/956,160  
CURRENT FILING DATE: 2004-10-04  
NUMBER OF SEQ ID NOS: 222274  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 123988  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-10-956-160-123988

Query Match 61.7%; Score 14.8; DB 11; Length 25;  
Best Local Similarity 72.2%; Pred. No. 7.5e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGGGCGUGGUUAGGCG 21  
|||||:|:|:|:|:|:|  
Db 8 GAGGACTGCTTAAGCG 25

RESULT 4  
US-10-709-691B-1378586/c  
Sequence 1378586, Application US/10709691B  
Publication No. US20070031843A1  
GENERAL INFORMATION:  
APPLICANT: ROSETTA GENOMICS LTD  
APPLICANT: Bentwich, Itzhak  
APPLICANT: Avniel, Amir  
TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
TITLE OF INVENTION: and Bacterial Associated Oligonucleotides and Uses Thereof  
FILE REFERENCE: Efs23  
CURRENT APPLICATION NUMBER: US/10/709,691B  
CURRENT FILING DATE: 2004-05-24  
NUMBER OF SEQ ID NOS: 4254815  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1378586  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Neisseria meningitidis Z2491  
US-10-709-691B-1378586

Query Match 60.0%; Score 14.4; DB 9; Length 17;  
Best Local Similarity 75.0%; Pred. No. 1.1e+04;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGGGCGUGGUUAGGCG 21  
|||||:|:|:|:|:|:|  
Db 17 GGGGCTGGTTACGGC 2

RESULT 5  
US-10-714-333A-1176587  
Sequence 1176587, Application US/10714333A  
Publication No. US20070031844A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/10/714,333A  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 1176587  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-714-333A-1176587

Query Match 59.2%; Score 14.2; DB 10; Length 19;  
Best Local Similarity 84.2%; Pred. No. 1.4e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGGGCGUGGUUAGGC 20  
|||||:|:|:|:|:|:|  
Db 1 GAGAGCAGCUGGUUAGGC 19

RESULT 6  
US-11-093-832-1176587  
Sequence 1176587, Application US/11093832  
Publication No. US20070039072A1  
GENERAL INFORMATION:  
APPLICANT: Dharmacon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/093,832  
CURRENT FILING DATE: 2005-03-29  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 1176587  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens

US-10-709-691B-123481/c

; SEQ ID NO 142124  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-709-691B-142124

Query Match 58.3%; Score 14; DB 9; Length 22;  
Best Local Similarity 78.6%; Pred. No. 1.8e+04;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGUUAAG 18  
|||||:|:|:|  
Db 16 AGGGGCTGGTTAAG 3

## RESULT 12

US-10-709-691B-145999/c  
; Sequence 145999, Application US/10709691B  
; Publication No. US20070031843A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Avniel, Amir  
; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
; FILE REFERENCE: Efs23  
; CURRENT APPLICATION NUMBER: US/10709,691B  
; CURRENT FILING DATE: 2004-05-24  
; NUMBER OF SEQ ID NOS: 4254815  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 145999  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-709-691B-145999

Query Match 58.3%; Score 14; DB 9; Length 22;  
Best Local Similarity 78.6%; Pred. No. 1.8e+04;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGUUAAG 18  
|||||:|:|:|  
Db 16 AGGGGCTGGTTAAG 3

## RESULT 13

US-10-709-691B-153005/c  
; Sequence 153005, Application US/10709691B  
; Publication No. US20070031843A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Avniel, Amir  
; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
; FILE REFERENCE: Efs23  
; CURRENT APPLICATION NUMBER: US/10709,691B  
; CURRENT FILING DATE: 2004-05-24  
; NUMBER OF SEQ ID NOS: 4254815  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 153005  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-709-691B-153005

Query Match 58.3%; Score 14; DB 9; Length 22;  
Best Local Similarity 78.6%; Pred. No. 1.8e+04;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGUUAAG 18  
|||||:|:~|:|  
Db 16 AGGGGCTGGTTAAG 3

## RESULT 14

US-10-709-691B-187400/c  
; Sequence 187400, Application US/10709691B  
; Publication No. US20070031843A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Avniel, Amir  
; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
; FILE REFERENCE: Efs23  
; CURRENT APPLICATION NUMBER: US/10709,691B  
; CURRENT FILING DATE: 2004-05-24  
; NUMBER OF SEQ ID NOS: 4254815  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 187400  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-709-691B-187400

Query Match 58.3%; Score 14; DB 9; Length 22;  
Best Local Similarity 78.6%; Pred. No. 1.8e+04;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGUUAAG 18  
|||||:|:|:|  
Db 16 AGGGGCTGGTTAAG 3

## RESULT 15

US-10-709-691B-197873/c  
; Sequence 197873, Application US/10709691B  
; Publication No. US20070031843A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSETTA GENOMICS LTD  
; APPLICANT: Bentwich, Itzhak  
; APPLICANT: Avniel, Amir  
; TITLE OF INVENTION: Bioinformatically Detectable Group of Novel Regulatory Bacterial  
; FILE REFERENCE: Efs23  
; CURRENT APPLICATION NUMBER: US/10709,691B  
; CURRENT FILING DATE: 2004-05-24  
; NUMBER OF SEQ ID NOS: 4254815  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 197873  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-709-691B-197873

Query Match 58.3%; Score 14; DB 9; Length 22;  
Best Local Similarity 78.6%; Pred. No. 1.8e+04;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGGCGUGUUAAG 18  
|||||:|:|:|  
Db 16 AGGGGCTGGTTAAG 3

Search completed: June 19, 2007, 13:30:34  
Job time : 612.5 secs



GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2007, 12:49:12 ; Search time 6876 Seconds  
(without alignments)  
216.548 Million cell updates/sec

Title: US-10-604-726A-6034

Perfect score: 24  
Sequence: 1 ugagagggcgguaagcggucc 24

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 35954

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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18: gb\_gss4.\*  
19: gb\_gss5.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	11.4	47.5	25	15	AZ794596
6	11.2	46.7	24	15	AZ341038
7	11.2	46.7	25	15	AZ820085
8	11	45.8	20	15	AZ846437
9	11	45.8	21	15	AZ493166
10	11	45.8	21	15	AZ836049
11	11	45.8	25	15	AZ945526
12	10.8	45.0	22	1	A1183338
13	10.6	44.2	20	15	AZ346729
14	10.6	44.2	25	15	AZ851549

C 15	10.4	43.3	19	15	AZ595016
C 16	10.4	43.3	22	1	AA978171
C 17	10.4	43.3	24	15	AZ786207
C 18	10.2	42.5	19	15	AZ331326
C 19	10.2	42.5	19	15	AZ345449
C 20	10.2	42.5	19	15	AZ345511
C 21	10.2	42.5	19	15	AZ345536
C 22	10.2	42.5	19	15	AZ345572
C 23	10.2	42.5	19	15	AZ346709
C 24	10.2	42.5	19	15	AZ346710
C 25	10.2	42.5	19	15	AZ368837
C 26	10.2	42.5	19	15	AZ447223
C 27	10.2	42.5	19	15	AZ447247
C 28	10.2	42.5	19	15	AZ510096
C 29	10.2	42.5	19	15	AZ510106
C 30	10.2	42.5	19	15	AZ638980
C 31	10.2	42.5	21	15	AZ495585
C 32	10.2	42.5	21	15	AZ510134
C 33	10.2	42.5	21	15	AZ645749
C 34	10.2	42.5	21	15	AZ850337
C 35	10.2	42.5	22	15	AZ785081
C 36	10	41.7	19	5	CA794263
C 37	10	41.7	20	15	AZ417235
C 38	10	41.7	22	15	AZ318425
C 39	10	41.7	22	15	AZ330040
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C 41	10	41.7	23	7	AW246048
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C 43	10	41.7	23	16	BH792606
C 44	10	41.7	25	15	AZ611099
C 45	10	41.7	25	15	AZ772979

#### ALIGNMENTS

RESULT 1  
LOCUS AZ806300  
DEFINITION 2M0068F13F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGC2M0068F13 F, genomic survey sequence.  
ACCESSION AZ806300  
VERSION AZ806300.1 GI:12967111  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0068 row: F column: 13  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers 1. .24  
/organism="Mus musculus"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0068F13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 52.5%; Score 12.6; DB 15; Length 24;
Best Local Similarity 57.9%; Pred. No. 7.7e+05;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UGAGAGGGCGUGGUUAGG 19
:|||||:|:|:|:|
Db 5 TGGAGTGGGTGGTTAGGG 23

RESULT 2
AI473941/c
LOCUS AI473941 22 bp mRNA linear EST 09-MAR-1999
DEFINITION tm04c11.x1 NCI CGAP Co14 Homo sapiens cDNA clone IMAGE:2155604 3, similar to TR:Q06459 Q06459 NUCLEOLIN. 1, mRNA sequence.
AI473941
ACCESSION AI473941.1 GI:4326986
VERSION AI473941.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source

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/db_xref="taxon:9606"
/clone="IMAGE:2155604"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Co14"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"

ORIGIN
Query Match 50.0%; Score 12; DB 1; Length 22;
Best Local Similarity 70.0%; Pred. No. 1.4e+06;
Matches 14; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAGAGGGCGUGGUUAGGCG 21
|||||:|:|:|
Db 20 CAGAGGGCGGAGTCGAGGGG 1

RESULT 3
R89803/c
LOCUS R89803 25 bp mRNA linear EST 24-AUG-1995
DEFINITION YP91b12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194783 5, similar to gb.X63526 ELONGATION FACTOR 1-GAMMA (HUMAN); mRNA sequence.
R89803
ACCESSION R89803.1 GI:954630
VERSION R89803.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maria, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1193
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1193 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 1.
Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3763833"
/db_xref="taxon:9606"
/clone="IMAGE:194783"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/notes="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dr) primer [5' AACTGGAAGAAATTAATAAGATCTTTTTTTTTTTTTTTT 3']"

```

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTV3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 50.0%; Score 12; DB 11; Length 25;  
Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGGCTGGTAA 17  
|||||:|:|:|  
Db 12 GGGGCTGGTAA 1

RESULT 4

AZ654730/C 21 bp DNA linear GSS 14-DEC-2000

LOCUS IM0529P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC1M0529P05 F, genomic survey sequence.

ACCESSION AZ654730

VERSION AZ654730.1 GI:11791876

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0529 row: P column: 05  
Seq primer: CGTTGTAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES

source

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0529P05"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 48.3%; Score 11.6; DB 15; Length 21;  
Best Local Similarity 66.7%; Pred. NO. 2.1e+06;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAGAGGGGCUUAGG 19  
|||||:|:|:|  
Db 19 GGGTGGGATGGTAAGG 2

RESULT 5

AZ794596 25 bp DNA linear GSS 16-FEB-2001

LOCUS 2M0048M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC2M0048M20 F, genomic survey sequence.

ACCESSION AZ794596

VERSION AZ794596.1 GI:12940723

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 25)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0048 row: M column: 20  
Seq primer: CGTTGTAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 25.

FEATURES

source

1..25

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0048M20"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 47.5%; Score 11.4; DB 15; Length 25;  
Best Local Similarity 57.1%; Pred. No. 2.6e+06;  
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 UGAGAGGCGGCUUUAAGGCG 21  
: ||||| : : : : :  
Db 5 TGGAGGCGGTGTGAGGGG 25

## RESULT 6

AZ341038/c 24 bp DNA linear GSS 29-SEP-2000  
LOCUS IM0073B16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0073B16 F, genomic survey sequence.

ACCESSION AZ341038.1 GI:10416890

VERSION

KEYWORDS

SOURCE

## ORGANISM

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0073 row: B column: 16

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

## FEATURES

## source

1. 24

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0073B16"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

## ORIGIN

Query Match 46.7%; Score 11.2; DB 15; Length 24;  
Best Local Similarity 69.8%; Pred. No. 3.2e+06;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 GGGCGGCUUUAAGGCG 21  
||||| : : : : :  
Db 18 GGGGATGGGTAAAGTG 3

## RESULT 7

## LOCUS

AZ820085/c 25 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0092001F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0092001 F, genomic survey sequence.

ACCESSION AZ820085

VERSION AZ820085.1 GI:12989993

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 25)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

## COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0092 row: O column: 01

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

## FEATURES

## source

1. 25

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0092001"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 46.7%; Score 11.2; DB 15; Length 25;  
Best Local Similarity 68.8%; Pred. No. 3.2e+06;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GGGGCGUGUUAAGGCG 21  
|||||:|||||  
Db 19 GGGGATGGTAAAGTG 4

## RESULT 8

AZ846437 20 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0146E10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0146E10 R, genomic survey sequence.

ACCESSION AZ846437  
VERSION AZ846437.1 GI:13016345  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0146 row: E column: 10

Seq primer: CACACAGAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 20.

## FEATURES

Location/Qualifiers

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0146E10"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 45.8%; Score 11; DB 15; Length 20;  
Best Local Similarity 57.9%; Pred. No. 3.9e+06;  
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 UGAGAGGGCGUGUUAAGG 19  
:|||||:|||||:|  
Db 2 TGGGATGGTGGGTAGGG 20

## RESULT 9

AZ493166 21 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0327K05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0327K05 R, genomic survey sequence.

ACCESSION AZ493166  
VERSION AZ493166.1 GI:10666413  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0327 row: K column: 05

Seq primer: CACACAGAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 21.

## FEATURES

Location/Qualifiers

1..21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0327K05"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 45.8%; Score 11; DB 15; Length 21;  
Best Local Similarity 57.9%; Pred. No. 3.9e+06;  
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 UGAGGGGGCGUUAAGG 19  
: ||||| : : : : :  
Db 2 TGGGAGTGGATGGGTAGG 20

## RESULT 10

AZ836049/c 21 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION 2M0130E11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0130E11 R, genomic survey sequence.

ACCESSION AZ836049  
VERSION 1  
KEYWORDS GI:13005957  
SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0130 row: E column: 11

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

## FEATURES

source

1..21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0130E11"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 45.8%; Score 11; DB 15; Length 21;  
Best Local Similarity 90.9%; Pred. No. 3.9e+06;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAGGGGCGUG 13  
: ||||| : : : : :  
Db 15 AGAGGGGCTGG 5

## RESULT 11

AZ945526 25 bp DNA linear GSS 26-APR-2001  
LOCUS  
DEFINITION 2M0206L22R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0206L22 R, genomic survey sequence.

ACCESSION AZ945526  
VERSION 1  
KEYWORDS GI:13809815  
SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0206 row: L column: 22

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 25.

## FEATURES

source

1..25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0206L22"  
/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

```

ORIGIN
Query Match          45.0%; Score 10.8; DB 1; Length 22;
Best Local Similarity 64.3%; Pred. No. 4.9e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 GAGAGGGGCGUGGU 15
      ||||| :||:
Db      17 GAGTGGGGTGGTT 4

RESULT 13
A2346729/c

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AZ346729	20 bp	DNA	linear	GSS 29-SEP-2000
LOCUS				
DEFINITION	IM0802A10F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0082A10 F, genomic survey sequence.			
ACCESSION	AZ346729			
VERSION	AZ346729.1	GI:10425966		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

REFERENCE  
AUTHORS

1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

mouse, whose genome scarring with paired end reads from 10X  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606

```

Tel: 801 585 5000
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: A column: 10
Seq primer: CATTGTAACACACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"

```

/clone="UUGC1M0082A10"  
 /sex="Male"  
 /lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

# ORIGIN

Query Match 44.2%; Score 10.6; DB 15; Length 20;  
 Best Local Similarity 64.7%; Pred. No. 5.9e+06;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 GAGAGGGGCGUGUUAAG 18  
 |||||:||||:  
 Db 20 GAGTGAGGTTGGTGAAG 4

# RESULT 14

AZ851549/c  
 LOCUS 25 bp DNA linear GSS 21-FEB-2001  
 DEFINITION 2M0153P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0153P13 R, genomic survey sequence.  
 ACCESSION AZ851549  
 VERSION AZ851549.1 GI:13037657  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 25)

REFERENCE  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Kelly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

UNPUBLISHED (2000)

JOURNAL  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0153 row: P column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

# FEATURES

source

1..25

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0153P13"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

# ORIGIN

Query Match 44.2%; Score 10.6; DB 15; Length 25;  
 Best Local Similarity 64.7%; Pred. No. 6e+06;  
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 AGAGGGGCGUGUUAAGG 19  
 |||||:||||:  
 Db 25 AGAGGTAAGGTTAAGG 9

# RESULT 15

AZ595016/c  
 LOCUS 19 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0407C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0407C19 F, genomic survey sequence.  
 ACCESSION AZ595016  
 VERSION AZ595016.1 GI:11717206  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Kelly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

UNPUBLISHED (2000)

JOURNAL  
 COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0407 row: C column: 19

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

# FEATURES

source

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0407C19"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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polynucleotide kinase. Adaptor oligonucleotides were

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inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into



adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 43.3%; Score 10.4; DB 15; Length 19;  
Best Local Similarity 75.0%; Pred. No. 7.3e+06;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UGAGAGGGGCTG 12  
: |||||:  
Db 17 TGGAGGGGCTG 6

Search completed: June 19, 2007, 20:24:43  
Job time : 6878 secs